

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 24, 2004, 06:47:52 ; Search time 328 Seconds
(without alignments)
575.173 Million cell updates/sec

Title: SEQ9-X-AT-5-9-16-39
Perfect score: 291
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2438257 seqs, 184957644 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database: Published.Applications.NA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 291 | 100.0 | 288 | 9 | US-09-759-584-58 | Sequence 58, Appl |
| 3 | 286 | 98.3 | 285 | 9 | US-09-829-381A-16 | Sequence 16, Appl |
| 4 | 286 | 98.3 | 414 | 9 | US-09-759-584-48 | Sequence 48, Appl |
| 5 | 286 | 98.3 | 414 | 13 | US-10-006-252A-19 | Sequence 19, Appl |
| 6 | 281 | 96.6 | 403 | 9 | US-09-732-561-13 | Sequence 13, Appl |
| 7 | 269 | 92.4 | 308 | 9 | US-09-829-381A-5 | Sequence 5, Appl |
| 8 | 261 | 89.7 | 243 | 9 | US-09-938-842A-2046 | Sequence 2046, Ap |
| 9 | 261 | 89.7 | 243 | 11 | US-09-938-842A-2046 | Sequence 2046, Ap |
| 10 | 261 | 89.7 | 400 | 9 | US-09-732-561-15 | Sequence 15, Appl |
| 11 | 261 | 89.7 | 400 | 9 | US-09-887-576-607 | Sequence 607, Appl |
| 12 | 261 | 89.7 | 1616 | 9 | US-09-732-561-21 | Sequence 21, Appl |
| 13 | 260 | 89.3 | 270 | 9 | US-09-829-381A-14 | Sequence 14, Appl |
| 14 | 260 | 89.3 | 286 | 9 | US-09-829-381A-12 | Sequence 12, Appl |
| 15 | 258 | 88.7 | 500 | 9 | US-09-829-381A-9 | Sequence 9, Appl |
| 16 | 211 | 72.5 | 284 | 9 | US-09-759-584-50 | Sequence 50, Appl |
| 17 | 201 | 69.1 | 306 | 9 | US-09-829-381A-8 | Sequence 8, Appl |
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| 19 | 160 | 55.0 | 158 | 14 | US-10-178-449A-34 | Sequence 34, Appl |
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| 22 | 160 | 55.0 | 658 | 14 | US-10-178-449A-7 | Sequence 7, Appl |
| 23 | 153 | 52.6 | 579 | 14 | US-10-178-449A-31 | Sequence 31, Appl |
| 24 | 150 | 51.5 | 150 | 9 | US-09-759-584-31 | Sequence 31, Appl |
| 25 | 150 | 51.5 | 529 | 14 | US-10-178-449A-48 | Sequence 48, Appl |
| 26 | 149.5 | 51.4 | 470 | 14 | US-10-178-213-88 | Sequence 88, Appl |
| 27 | 147 | 50.5 | 150 | 9 | US-09-759-584-34 | Sequence 34, Appl |
| 28 | 146 | 50.2 | 439 | 14 | US-10-178-449A-15 | Sequence 15, Appl |
| 29 | 146 | 50.2 | 457 | 14 | US-10-178-449A-13 | Sequence 13, Appl |
| 30 | 146 | 50.2 | 458 | 14 | US-10-178-449A-21 | Sequence 21, Appl |
| 31 | 146 | 50.2 | 460 | 14 | US-10-178-449A-17 | Sequence 17, Appl |
| 32 | 146 | 50.2 | 461 | 14 | US-10-178-449A-46 | Sequence 46, Appl |
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| 34 | 146 | 50.2 | 464 | 14 | US-10-178-449A-19 | Sequence 19, Appl |
| 35 | 146 | 50.2 | 472 | 14 | US-10-178-449A-23 | Sequence 23, Appl |
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| 37 | 145 | 49.8 | 150 | 9 | US-09-759-584-33 | Sequence 33, Appl |
| 38 | 145 | 49.8 | 460 | 14 | US-10-178-449A-3 | Sequence 3, Appl |
| 39 | 145 | 49.8 | 503 | 14 | US-10-178-449A-25 | Sequence 25, Appl |
| 40 | 138 | 47.4 | 499 | 14 | US-10-178-449A-27 | Sequence 27, Appl |
| 41 | 138 | 47.4 | 517 | 14 | US-10-178-449A-36 | Sequence 36, Appl |
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| 43 | 109.5 | 37.6 | 564 | 9 | US-09-777-347-2 | Sequence 2, Appl |
| 44 | 109.5 | 37.6 | 3528 | 9 | US-09-777-347-2 | Sequence 127, Appl |
| 45 | 103.5 | 35.6 | 476 | 14 | US-10-178-213-127 | Sequence 127, Appl |

ALIGNMENTS

RESULT 1
US-09-829-381A-17
Sequence 17, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenthal, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSES: Charles E. Cohen, Monsanto Company, BR4F
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/829,381A
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-829-381A-17

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Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 9

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QY 1 GlnlyLeuCyS***ArGProSeR***ThTTPSeRGIyValCyS***AsnAsnAsnAla 20
Db 118 CAAAGTGTGGCAAGGCGCATGCTGTCAGAGCTGCGGAAACAACAGCGCA 177
QY 21 CysLyAsnGlnCyS11eArGLeuGlnLySAlaArGHiSGlySeRCysAsnTyR***Phe 40
Db 178 TGCAGAACCAATGATCATGACTCGAAGGCGCATGATCTTGCAACTAGCTCTTC 237
QY 41 ProAlaHisLyCyS11eCyS11eCySTyRPhProCyS 51
Db 238 CCAGCTCACAGTGCATCTGCTACTTTCATC 270

RESULT 2
US-09-759-584-58
Sequence 58, Application US/09759584
Patent No. US20010014732A1
GENERAL INFORMATION:
APPLICANT: BROEKERT, WILLEM F.
APPLICANT: CAMUDE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,667
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-822-0944
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 43..282
US-09-759-584-58

Alignment Scores:
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Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 9

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QY 21 CysLyAsnGlnCyS11eArGLeuGlnLySAlaArGHiSGlySeRCysAsnTyR***Phe 40
Db 190 TGCAGAACCAATGATCATGACTCGAAGGCGCATGATCTTGCAACTAGCTCTTC 249
QY 41 ProAlaHisLyCyS11eCyS11eCySTyRPhProCyS 51
Db 250 CCAGCTCACAGTGCATCTGCTACTTTCCTTGT 282

RESULT 3
US-09-829-381A-16
Sequence 16, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Mu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Charles E. Cohen, Monsanto Company, B44F
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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 Query Match: 98.28% Indels: 0
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 Db 103 CAGAGGTGTGCGAAGGCCAAGTGGACATGTCAGAGCTGTGGAAACAATAAGCA 162
 QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTrp***Phe 40
 Db 163 TGCAGAGTCTGTCATTAACCTTGAGAAAGCACAGACATGATCTTGCAACTATGCTTC 222
 QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
 Db 223 CCAGCTCAACAAGTGTATCTGCTACTTCCCTGT 255

RESULT 6

US-09-732-561-13
 Sequence 13, Application US/09732561
 Patent No. US20020035738A1

GENERAL INFORMATION:

APPLICANT: Thomma, Bart
 APPLICANT: Terras, Franky
 APPLICANT: Penninckx, Iris
 APPLICANT: Manners, John
 APPLICANT: Kazan, Kemal
 APPLICANT: Broekaert, Willem
 TITLE OF INVENTION: Plant Protection Method
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: ZENECA Ag Products
 STREET: 1800 Concord Pike
 CITY: Wilmington
 STATE: DE
 COUNTRY: USA
 ZIP: 19850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/732,561
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/202,638
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB97/01672
 FILING DATE: 20-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hobenschutz, Liza D.
 REGISTRATION NUMBER: 33,712
 REFERENCE/DOCKET NUMBER: PPD 50165/UST
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (302) 886-1699
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 403 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 STRAIN: PDF 1.1
 US-09-732-561-13

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 Query Match: 96.56% Indels: 0
 DB: 9 Gaps: 0

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 QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTrp***Phe 40
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 QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
 Db 233 CCAGCTCAACAAGTGTATCTGCTACTTCCCATGT 265

RESULT 7

US-09-829-381A-5
 Sequence 5, Application US/09829381A
 Patent No. US20020144306A1

GENERAL INFORMATION:

APPLICANT: Liang, Jihong
 Wu, Yonnie S.
 Rosenberger, Cindy A.
 TITLE OF INVENTION: Antifungal Polypeptide and Methods for
 Controlling Plant Pathogenic Fungi
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Charles E. Cohen, Monsanto Company, BtAF
 STREET: 700 Chesterfield Village Parkway No. US20020144306A1ch
 CITY: St. Louis
 STATE: Missouri
 COUNTRY: USA
 ZIP: 63198
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/829,381A
 FILING DATE: 09-Apr-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/103,489
 FILING DATE: 1998-06-24
 ATTORNEY/AGENT INFORMATION:
 NAME: Cohen, Charles E.
 REGISTRATION NUMBER: 34,565
 REFERENCE/DOCKET NUMBER: 38-21 (10700)A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 537-6224
 TELEFAX: (314) 537-6047
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 308 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-829-381A-5

Alignment Scores:

Pred. No.: 1.56e-27 Length: 308
 Score: 269.00 Matches: 43

Percent Similarity: 94.12%
Best Local Similarity: 84.31%
Query Match: 92.44%
DB: 9

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QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
Db 156 CGGAAGTTGTGCGAGAGTCCAAAGTGAACATGTCAGGGGTGTGTGGAAACAACATGCT 215
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 216 TGAAGAATCAGTGCATTAACTTGAAGGCGACATGATCTTGCACATGTCCTTC 275
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 276 CCAGCTCACAGTGCATATGCTACTTCCCTGT 308

RESULT 8

US-09-938-842A-2046
; Sequence 2046, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2046
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2046

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Score: 261.00 Matches: 41
Percent Similarity: 94.12% Conservative: 7
Best Local Similarity: 80.39% Mismatches: 3
Query Match: 89.69% Indels: 0
DB: 9 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-938-842A-2046 (1-243)

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Db 88 CAGAAGTTGTGCGAGAGTCCAAAGTGAACATGTCAGGGGTGTGTGGAAACAACATGCA 147
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 148 TGAAGAATCAGTGCATTAACTTGAAGGCGACATGATCTTGCACATGTCCTTC 207

QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 208 CCAGCACACAAGTGTATCTGTTACCTCCCATGT 240

RESULT 9

US-09-938-842A-2046
; Sequence 2046, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2046
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2046

Alignment Scores:
Pred. No.: 1,38e-26 Length: 243
Score: 261.00 Matches: 41
Percent Similarity: 94.12% Conservative: 7
Best Local Similarity: 80.39% Mismatches: 3
Query Match: 89.69% Indels: 0
DB: 11 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-938-842A-2046 (1-243)

QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
Db 88 CAGAAGTTGTGCGAGAGTCCAAAGTGAACATGTCAGGGGTGTGTGGAAACAACATGCA 147
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 148 TGAAGAATCAGTGCATTAACTTGAAGGCGACATGATCTTGCACATGTCCTTC 207
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 208 CCAGCACACAAGTGTATCTGTTACCTCCCATGT 240

RESULT 10

US-09-732-561-15
; Sequence 15, Application US/09732561
; Patent No. US20020035738A1
; GENERAL INFORMATION:

; APPLICANT: Thoma, Bart
; APPLICANT: Terras, Franky
; APPLICANT: Penninckx, Iris
; APPLICANT: Manners, John
; APPLICANT: Kazan, Kemal
; APPLICANT: Broekaert, Willem
; TITLE OF INVENTION: Plant Protection Method
; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Ag Products
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,561
; FILING DATE:
; CLASSIFICATION:


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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Arabidopsis PDF1.2 gene
; INDIVIDUAL ISOLATE: DNA sequence Figure 14
US-09-732-561-21

Alignment Scores:
Pred. No.: 1,99e-25 Length: 1616
Score: 261.00 Matches: 41
Percent Similarity: 94.12% Conservative: 7
Best Local Similarity: 80.39% Mismatches: 3
Query Match: 89.69% Indels: 0
DB: 9 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-732-561-21 (1-1616)

QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
Db 1412 CAGAGTGTGCGAGAGCCAAAGTGGGACATGGTCAGGGGTTTCGGGAAACAGTAATGCA 1471
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 1472 TGCAGAAATCATGTCATTACCTCGAAGAGCCAAACATGGATCATGCAACTATGTCTTC 1531
QY 41 ProlahisLysCysIleCysTyrPheProCys 51
Db 1532 CCAGCACAAAGTGTATCTGTACGTCCCATGT 1564

RESULT 13
US-09-829-381A-14
; Sequence 14, Application US/09829381A
; Patent No. US20020144306A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Shah, Dilip M.
; Wu, Yennie S.
; Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,381A
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; INFORMATION FOR SEQ ID NO: 14:
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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-829-381A-14

Alignment Scores:
Pred. No.: 2,2e-26 Length: 270
Score: 260.00 Matches: 40
Percent Similarity: 94.00% Conservative: 7
Best Local Similarity: 80.00% Mismatches: 3
Query Match: 89.35% Indels: 0
DB: 9 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-829-381A-14 (1-270)

QY 2 LysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAlaCys 21
Db 109 AGTGTGGGAGAGACCAAGTGGGACATGGTCAGAGTTTGGGACACACATGCAATGC 168
QY 22 LysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***PhePro 41
Db 169 AGGAACCAATGAGAAACCTTGAAGAGCAGAACACGATCTTGCACACTATGTCTTCCA 228
QY 42 AlaHisLysCysIleCysTyrPheProCys 51
Db 229 GCTCACAATGTATTGTACTTCCCATGT 258

RESULT 14
US-09-829-381A-12
; Sequence 12, Application US/09829381A
; Patent No. US20020144306A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Shah, Dilip M.
; Wu, Yennie S.
; Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,381A
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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US-09-829-381A-12
Alignment Scores:
Pred. No.: 2.38e-26 Length: 286
Score: 260.00 Matches: 40
Percent Similarity: 94.00% Conservative: 7
Best Local Similarity: 80.00% Mismatches: 3
Query Match: 89.35% Indels: 0
DB: 9 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-829-381A-12 (1-286)
QY 2 LysLeuCyS***ArgProSer***ThrTrpSerGlyValCyS***AsnAsnAlaCyS 21
Db 117 AGTTGTCGAGACCAAGTGGACATGTCAGAGTTTGTGGACACACATGCAATGC 176
QY 22 LysAsnGlnCySIIeArgLeuGluLysAlaArgHisGlySerCySAsnTyr***PhePro 41
Db 177 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGCGATCTTGCAACTATGTCCTCCA 236
QY 42 AlaHisLysCySIIeCysTyrPheProCys 51
Db 237 GCTCAAAATGTAATTTGTTACTTCCATGT 266

RESULT 15
US-09-829-381A-9
; Sequence 9, Application US/09829381A
; Patent No. US20020144306A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Wu, Yennie S.
; Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BBAF
; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,381A
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 500 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-829-381A-9
Alignment Scores:
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```
Pred. No.: 9.81e-26 Length: 500
Score: 258.00 Matches: 40
Percent Similarity: 92.16% Conservative: 7
Best Local Similarity: 78.43% Mismatches: 4
Query Match: 88.66% Indels: 0
DB: 9 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-829-381A-9 (1-500)
QY 1 GlnLysLeuCyS***ArgProSer***ThrTrpSerGlyValCyS***AsnAsnAla 20
Db 156 CGGAAGTTGTCGAGAGTCCAAGTGGACATGTCAGCGTGTGTGGGAATAATAACGCA 215
QY 21 CysLysAsnGlnCySIIeArgLeuGluLysAlaArgHisGlySerCySAsnTyr***Phe 40
Db 216 TGCAGAACCAATGCAAAACCTTGAAGAGCAGACACGCGATCTTGCAACTATGTCCTTC 275
QY 41 ProAlaHisLysCySIIeCysTyrPheProCys 51
Db 276 CCAGCTCACAAATGTAATTTGTTACTTCCATGT 308
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Search completed: March 24, 2004, 09:17:33
Job time : 342 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 24, 2004, 05:43:48 ; Search time 3189 seconds
(without alignments)
477,570 Million cell updates/sec

Title: SEQ9-X-AT-5-9-16-39
Perfect score: 291
Sequence: 1 QKLCXSPSXTWVGVCXNNNA.....RGGSCNYCFPAHKICICVPCF 51

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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-DB=EST -OPMT=fastcap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: em_esthum:*
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8: em_hcc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_eston:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
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27: em_gss_vrl:*
28: gb_gssl:*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 2 | 291 | 100.0 | 425 | 14 | CD834852 | CD834852 BN45.043G |
| 3 | 291 | 100.0 | 427 | 14 | CD833613 | CD833613 BN40.067P |
| 4 | 291 | 100.0 | 449 | 14 | CD833047 | CD833047 BN40.065M |
| 5 | 291 | 100.0 | 457 | 14 | CD831226 | CD831226 BN40.058J |
| 6 | 291 | 100.0 | 473 | 14 | CD834995 | CD834995 BN45.043O |
| 7 | 291 | 100.0 | 476 | 14 | CD833784 | CD833784 BN45.001I |
| 8 | 291 | 100.0 | 476 | 14 | CD834092 | CD834092 BN45.040I |
| 9 | 291 | 100.0 | 481 | 14 | CD833924 | CD833924 BN45.040A |
| 10 | 291 | 100.0 | 482 | 14 | CD833627 | CD833627 BN45.001A |
| 11 | 291 | 100.0 | 523 | 14 | CD833661 | CD833661 BN45.001C |
| 12 | 291 | 100.0 | 543 | 14 | CD828840 | CD828840 BN40.040A |
| 13 | 291 | 100.0 | 646 | 14 | CD829429 | CD829429 BN40.042B |
| 14 | 291 | 100.0 | 762 | 28 | BZ517729 | BZ517729 BOMSG6TF |
| 15 | 287 | 98.6 | 522 | 14 | CD833938 | CD833938 BN45.040A |
| 16 | 287 | 98.6 | 543 | 14 | CD829085 | CD829085 BN40.041A |
| 17 | 286 | 98.3 | 408 | 14 | CD833779 | CD833779 BN45.001I |
| 18 | 286 | 98.3 | 409 | 14 | CD834090 | CD834090 BN45.040I |
| 19 | 286 | 98.3 | 418 | 14 | CD832625 | CD832625 BN40.064A |
| 20 | 286 | 98.3 | 419 | 14 | CD834168 | CD834168 BN45.040N |
| 21 | 286 | 98.3 | 420 | 14 | CD833944 | CD833944 BN45.040B |
| 22 | 286 | 98.3 | 421 | 14 | CD826491 | CD826491 BN45.064A |
| 23 | 286 | 98.3 | 421 | 14 | CD831111 | CD831111 BN40.058A |
| 24 | 286 | 98.3 | 421 | 14 | CD833977 | CD833977 BN45.040D |
| 25 | 286 | 98.3 | 422 | 14 | CD833983 | CD833983 BN45.040D |
| 26 | 286 | 98.3 | 426 | 14 | CD827413 | CD827413 BN25.067G |
| 27 | 286 | 98.3 | 438 | 14 | CD831294 | CD831294 BN40.058N |
| 28 | 286 | 98.3 | 438 | 14 | CD831479 | CD831479 BN40.059J |
| 29 | 286 | 98.3 | 446 | 14 | CD834068 | CD834068 BN45.040H |
| 30 | 286 | 98.3 | 447 | 14 | CD832592 | CD832592 BN40.063O |
| 31 | 286 | 98.3 | 450 | 14 | CD834611 | CD834611 BN45.042H |
| 32 | 286 | 98.3 | 452 | 14 | CD832071 | CD832071 BN40.061O |
| 33 | 286 | 98.3 | 453 | 14 | CD834008 | CD834008 BN45.040E |
| 34 | 286 | 98.3 | 458 | 14 | CD834994 | CD834994 BN45.043O |
| 35 | 286 | 98.3 | 470 | 14 | CD831680 | CD831680 BN40.060H |
| 36 | 286 | 98.3 | 480 | 14 | CD828332 | CD828332 BN25.070H |
| 37 | 286 | 98.3 | 543 | 14 | CD830628 | CD830628 BN40.046D |
| 38 | 286 | 98.3 | 553 | 14 | CD831014 | CD831014 BN40.047K |
| 39 | 286 | 98.3 | 803 | 28 | BH458392 | BH458392 BOGW36TF |
| 40 | 282 | 96.9 | 457 | 14 | CD831392 | CD831392 BN40.059D |
| 41 | 281 | 96.6 | 318 | 9 | AA713157 | AA713157 32717 Lam |
| 42 | 281 | 96.6 | 421 | 9 | AV816118 | AV816118 AV816118 |
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| 44 | 280 | 96.2 | 448 | 14 | CD837568 | CD837568 BN45.052M |
| 45 | 277 | 95.2 | 421 | 14 | CD837517 | CD837517 BN45.052I |

ALIGNMENTS

RESULT 1
CD832294
LOCUS
DEFINITION
CD832294.1 GI:32514234
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

CD832294
BN40.062L22F011227 BN40 Brassica napus cDNA clone BN40062L22, mRNA
sequence.
CD832294
CD832294.1 GI:32514234
EST.
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 409)
Genoplatte, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com)
and http://genoplatte-info.infobiogen.fr.
Location/Qualifiers
source
1..409
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40062L22"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN
Alignment Scores:
Pred. No.: 7,67e-23 Length: 409
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x CD832294 (1-409)

QY 1 GlnLysLeuCyS***ArgProSer***ThrTrpSerGlyValCyS***AsnAsnAsnAla 20
Db 138 CAGAAGCTGTGGAAAGGCAAGTGGAGCTGTGGAGTCTGTGGAAACAATAATGCA 197
QY 21 CysLysAsnGlnCysIleArgLeuGlnLysAlaArgHisGlySerCysAsnTy***Phe 40
Db 198 TCGAAGATCAGTGCATTCGACTAGAGAAAGCACACATGGATCTTGGCACTATGCTTC 257
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 258 CCAGCTCACAGTGCATCTGCTACTTCCTTGT 290

RESULT 2
CD834852 425 bp mRNA linear EST 10-JUL-2003
LOCUS
DEFINITION
BN45.043G08F011229 BN45 Brassica napus cDNA clone BN45043G08, mRNA
sequence.
ACCESSION
CD834852
VERSION
CD834852.1 GI:32516792
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
1 (bases 1 to 425)
AUTHORS
Genoplatte, a major partnership french program in plant genomics
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com)
and http://genoplatte-info.infobiogen.fr.
Location/Qualifiers
source
1..425
/organism="Brassica napus"

FEATURES
source
1..425
/mol_type="mRNA"
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/db_xref="taxon:3708"
/clone="BN40067P16"
/tissue_type="seed"
/clone_lib="BN40"

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/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45043G08"
/tissue_type="seed"
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ORIGIN
Alignment Scores:
Pred. No.: 8.1e-23 Length: 425
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x CD834852 (1-425)

QY 1 GlnLysLeuCyS***ArgProSer***ThrTrpSerGlyValCyS***AsnAsnAsnAla 20
Db 136 CAGAAGCTGTGGAAAGGCAAGTGGAGCTGTGGAGTCTGTGGAAACAATAATGCA 195
QY 21 CysLysAsnGlnCysIleArgLeuGlnLysAlaArgHisGlySerCysAsnTy***Phe 40
Db 196 TCGAAGATCAGTGCATTCGACTAGAGAAAGCACACATGGATCTTGGCACTATGCTTC 255
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 256 CCAGCTCACAGTGCATCTGCTACTTCCTTGT 288

RESULT 3
CD833613 427 bp mRNA linear EST 10-JUL-2003
LOCUS
DEFINITION
BN40.067P16F011228 BN40 Brassica napus cDNA clone BN40067P16, mRNA
sequence.
ACCESSION
CD833613
VERSION
CD833613.1 GI:32515553
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
1 (bases 1 to 427)
AUTHORS
Genoplatte, a major partnership french program in plant genomics
TITLE
Unpublished (2003)
JOURNAL
COMMENT
Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com)
and http://genoplatte-info.infobiogen.fr.
Location/Qualifiers
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1..427
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40067P16"
/tissue_type="seed"
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FEATURES
source
1..427
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40067P16"
/tissue_type="seed"
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ORIGIN
Alignment Scores:
Pred. No.: 8.16e-23 Length: 427
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

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SEQ9-X-AT-5-9-16-39 (1-51) x CD833613 (1-427)
QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
Db 138 CAGAAGCTGTGCGAAAGGCCAAGTGGACGCTGTGTGAGGAGTCTGTGGAAACAATAATGCA 197
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 198 TGCAGAAATCAGTGCATTCGATCAGAGAAAGCAGACATGGATCTTGCACATATGCTTTC 257
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 258 CCAGCTCACAAAGTGCATCTGCTACTTCCCTTGT 290

RESULT 4
CD833047
LOCUS
DEFINITION
  BN40.065M05F011229 BN40 Brassica napus cDNA clone BN40065M05, mRNA
  sequence.
ACCESSION
  CD833047.1 GI:32514987
VERSION
  CD833047
KEYWORDS
  EST.
SOURCE
  Brassica napus (rape)
ORGANISM
  Brassica napus
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 449)
AUTHORS
  Genoplatte, a major partnership french program in plant genomics
  Unpublished (2003)
JOURNAL
  Contact: Genoplatte
COMMENT
  Genoplatte
  93, rue Henri Rochefort 91025 EVRY CEDEX France
  Tel: 33 1 69 47 54 00
  Fax: 33 1 69 47 54 10
  This sequence has been generated in the framework of the french
  plant genomics programme 'Genoplatte' (http://www.genoplatte.com
  and http://genoplatte-info.infobiogen.fr).
  Location/Qualifiers
    source
      1..449
        /organism="Brassica napus"
        /mol_type="mRNA"
        /cultiVar="Jet neuf"
        /db_xref="taxon:3708"
        /clone="BN40065M05"
        /tissue_type="seed"
        /clone_lib="BN40"

FEATURES
  Alignment Scores:
    Pred. No.: 8,766-23 Length: 449
    Score: 291.00 Matches: 47
    Percent Similarity: 100.00% Conservative: 4
    Best Local Similarity: 92.16% Mismatches: 0
    Query Match: 100.00% Indels: 0
    DB: 14 Gaps: 0

ORIGIN
  SEQ9-X-AT-5-9-16-39 (1-51) x CD833047 (1-449)
  QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
  Db 119 CAGAAGCTGTGCGAAAGGCCAAGTGGACGCTGTGTGAGGAGTCTGTGGAAACAATAATGCA 178
  QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
  Db 179 TGCAGAAATCAGTGCATTCGATCAGAGAAAGCAGACATGGATCTTGCACATATGCTTTC 238
  QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
  Db 239 CCAGCTCACAAAGTGCATCTGCTACTTCCCTTGT 271

SEQ9-X-AT-5-9-16-39 (1-51) x CD833613 (1-427)
QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
Db 138 CAGAAGCTGTGCGAAAGGCCAAGTGGACGCTGTGTGAGGAGTCTGTGGAAACAATAATGCA 197
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 198 TGCAGAAATCAGTGCATTCGATCAGAGAAAGCAGACATGGATCTTGCACATATGCTTTC 257
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 258 CCAGCTCACAAAGTGCATCTGCTACTTCCCTTGT 290

RESULT 5
CD831226
LOCUS
DEFINITION
  BN40.058J10F011019 BN40 Brassica napus cDNA clone BN40058J10, mRNA
  sequence.
ACCESSION
  CD831226
VERSION
  CD831226.1 GI:32513166
KEYWORDS
  EST.
SOURCE
  Brassica napus (rape)
ORGANISM
  Brassica napus
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 457)
AUTHORS
  Genoplatte, a major partnership french program in plant genomics
  Unpublished (2003)
JOURNAL
  Contact: Genoplatte
COMMENT
  Genoplatte
  93, rue Henri Rochefort 91025 EVRY CEDEX France
  Tel: 33 1 69 47 54 00
  Fax: 33 1 69 47 54 10
  This sequence has been generated in the framework of the french
  plant genomics programme 'Genoplatte' (http://www.genoplatte.com
  and http://genoplatte-info.infobiogen.fr).
  Location/Qualifiers
    source
      1..457
        /organism="Brassica napus"
        /mol_type="mRNA"
        /cultiVar="Jet neuf"
        /db_xref="taxon:3708"
        /clone="BN40058J10"
        /tissue_type="seed"
        /clone_lib="BN40"

FEATURES
  Alignment Scores:
    Pred. No.: 8,996-23 Length: 457
    Score: 291.00 Matches: 47
    Percent Similarity: 100.00% Conservative: 4
    Best Local Similarity: 92.16% Mismatches: 0
    Query Match: 100.00% Indels: 0
    DB: 14 Gaps: 0

ORIGIN
  SEQ9-X-AT-5-9-16-39 (1-51) x CD831226 (1-457)
  QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
  Db 138 CAGAAGCTGTGCGAAAGGCCAAGTGGACGCTGTGTGAGGAGTCTGTGGAAACAATAATGCG 197
  QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
  Db 198 TGCAGAAATCAGTGCATTCGATCAGAGAAAGCAGACATGGATCTTGCACATATGCTTTC 257
  QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
  Db 258 CCAGCTCACAAAGTGCATCTGCTACTTCCCTTGT 290

RESULT 6
CD834995
LOCUS
DEFINITION
  BN45.043O08F011229 BN45 Brassica napus cDNA clone BN45043O08, mRNA
  sequence.
ACCESSION
  CD834995
VERSION
  CD834995.1 GI:32516935
KEYWORDS
  EST.
SOURCE
  Brassica napus (rape)
ORGANISM
  Brassica napus
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 473)
AUTHORS
  Genoplatte.

```

TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).
Location/Qualifiers
1..473
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN4504008"
/tissue_type="seed"
/clone_lib="BN45"

Alignment Scores: 9.44e-23 Length: 473
Pred. No.: 291.00 Matches: 47
Score: 291.00 Conservative: 4
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 92.16% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 14

SEQ9-X-AT-5-9-16-39 (1-51) x CD834995 (1-473)

QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAla 20
Db 156 CAGAAAGTTGTGTGAGAGCCAAAGTGGACATGTCAGGAGTTGTGGAAACAATAATGCG 215
QY 21 CysLysAsnGlnCysIleArgLeuGlnLysAlaArgHisGlySerCysAsnTy***Phe 40
Db 216 TGTAAAGATCATGTCATTCGATTCGAGAAAGCAGCATGATCTTGCAACTATGCTTC 275
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 276 CCAGCTCACAGTGTATCTGCTATTTCCCTTGT 308

RESULT 7
CD833784
LOCUS BN45.001122F010914 BN45 Brassica napus cDNA clone BN45001122, mRNA
DEFINITION sequence.
ACCESSION CD833784.1 GI:32515724
VERSION
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 476)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).
Location/Qualifiers
1..476
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"

SEQ9-X-AT-5-9-16-39 (1-51) x CD834995 (1-473)

QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAla 20
Db 156 CAGAAAGTTGTGTGAGAGCCAAAGTGGACATGTCAGGAGTTGTGGAAACAATAATGCG 215
QY 21 CysLysAsnGlnCysIleArgLeuGlnLysAlaArgHisGlySerCysAsnTy***Phe 40
Db 216 TGTAAAGATCATGTCATTCGATTCGAGAAAGCAGCATGATCTTGCAACTATGCTTC 275
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 276 CCAGCTCACAGTGTATCTGCTATTTCCCTTGT 308

RESULT 7
CD833784
LOCUS BN45.001122F010914 BN45 Brassica napus cDNA clone BN45001122, mRNA
DEFINITION sequence.
ACCESSION CD833784.1 GI:32515724
VERSION
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 476)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).
Location/Qualifiers
1..476
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"

FEATURES
source
1..476
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"

ORIGIN
Alignment Scores: 9.53e-23 Length: 476
Pred. No.: 291.00 Matches: 47
Score: 291.00 Conservative: 4
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 92.16% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 14

SEQ9-X-AT-5-9-16-39 (1-51) x CD834092 (1-476)

QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAla 20
Db 157 CAGAAAGTTGTGTGAGAGCCAAAGTGGACATGTCAGGAGTTGTGGAAACAATAATGCG 216
QY 21 CysLysAsnGlnCysIleArgLeuGlnLysAlaArgHisGlySerCysAsnTy***Phe 40
Db 217 TGTAAAGATCATGTCATTCGATTCGAGAAAGCAGCATGATCTTGCAACTATGCTTC 276

/db_xref="taxon:3708"
/clone="BN45001122"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Alignment Scores: 9.53e-23 Length: 476
Pred. No.: 291.00 Matches: 47
Score: 291.00 Conservative: 4
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 92.16% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 14

SEQ9-X-AT-5-9-16-39 (1-51) x CD833784 (1-476)

QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAla 20
Db 157 CAGAAAGTTGTGTGAGAGCCAAAGTGGACATGTCAGGAGTTGTGGAAACAATAATGCG 216
QY 21 CysLysAsnGlnCysIleArgLeuGlnLysAlaArgHisGlySerCysAsnTy***Phe 40
Db 217 TGTAAAGATCATGTCATTCGATTCGAGAAAGCAGCATGATCTTGCAACTATGCTTC 276
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 277 CCAGCTCACAGTGTATCTGCTATTTCCCTTGT 309

RESULT 8
CD834092
LOCUS BN45.040123F011018 BN45 Brassica napus cDNA clone BN45040123, mRNA
DEFINITION sequence.
ACCESSION CD834092.1 GI:32516032
VERSION
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 476)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and [http://www.genoplante-info.infobiogen.fr](http://genoplante-info.infobiogen.fr)).
Location/Qualifiers
1..476
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45040123"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Alignment Scores: 9.53e-23 Length: 476
Pred. No.: 291.00 Matches: 47
Score: 291.00 Conservative: 4
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 92.16% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 14

SEQ9-X-AT-5-9-16-39 (1-51) x CD834092 (1-476)

QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAla 20
Db 157 CAGAAAGTTGTGTGAGAGCCAAAGTGGACATGTCAGGAGTTGTGGAAACAATAATGCG 216
QY 21 CysLysAsnGlnCysIleArgLeuGlnLysAlaArgHisGlySerCysAsnTy***Phe 40
Db 217 TGTAAAGATCATGTCATTCGATTCGAGAAAGCAGCATGATCTTGCAACTATGCTTC 276
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 277 CCAGCTCACAGTGTATCTGCTATTTCCCTTGT 309

FEATURES
source
1..476
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45040123"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Alignment Scores: 9.53e-23 Length: 476
Pred. No.: 291.00 Matches: 47
Score: 291.00 Conservative: 4
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 92.16% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 14

SEQ9-X-AT-5-9-16-39 (1-51) x CD834092 (1-476)

QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAla 20
Db 157 CAGAAAGTTGTGTGAGAGCCAAAGTGGACATGTCAGGAGTTGTGGAAACAATAATGCG 216
QY 21 CysLysAsnGlnCysIleArgLeuGlnLysAlaArgHisGlySerCysAsnTy***Phe 40
Db 217 TGTAAAGATCATGTCATTCGATTCGAGAAAGCAGCATGATCTTGCAACTATGCTTC 276

QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
 Db 157 CAGAAGTTGTGTGAGAGGCCAAGTGGGACATGTCAGGAGTTTGTGGAACAATAATGCG 216
 QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
 Db 217 TGTAAAGATCAGTGCATTCGATTCGAAAGACACATGATCTTGCACATATGCTTC 276
 QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
 Db 277 CCAGCTCACAAGTGTATCTGCTATTTCCCTTGT 309

RESULT 9
 CD833924 481 bp mRNA linear EST 10-JUL-2003
 LOCUS DEFINITION BN45.040A03F011018 BN45 Brassica napus cDNA clone BN45040A03, mRNA
 sequence.
 CD833924
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Brassica napus (rape)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 481)
 Genoplatte.
 Genoplatte, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplatte
 Genoplatte
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>
 and <http://genoplatte-info.infobiogen.fr>).
 Location/Qualifiers
 1..481
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45040A03"
 /tissue_type="seed"
 /clone_lib="BN45"

ORIGIN
 Alignment Scores:
 Pred. No.: 9.67e-23 Length: 481
 Score: 291.00 Matches: 47
 Percent Similarity: 100.00% Conservative: 4
 Best Local Similarity: 92.16% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x CD833924 (1-481)
 QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
 Db 156 CAGAAGTTGTGTGAGAGGCCAAGTGGGACATGTCAGGAGTTTGTGGAACAATAATGCG 215
 QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
 Db 216 TGTAAAGATCAGTGCATTCGATTCGAAAGACACATGATCTTGCACATATGCTTC 275
 QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
 Db 276 CCAGCTCACAAGTGTATCTGCTATTTCCCTTGT 308

RESULT 10
 CD833627

LOCUS
 DEFINITION BN45.001A11F010914 BN45 Brassica napus cDNA clone BN45001A11, mRNA
 sequence.
 CD833627
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Brassica napus (rape)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 482)
 Genoplatte.
 Genoplatte, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplatte
 Genoplatte
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>
 and <http://genoplatte-info.infobiogen.fr>).
 Location/Qualifiers
 1..482
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45001A11"
 /tissue_type="seed"
 /clone_lib="BN45"

ORIGIN
 Alignment Scores:
 Pred. No.: 9.7e-23 Length: 482
 Score: 291.00 Matches: 47
 Percent Similarity: 100.00% Conservative: 4
 Best Local Similarity: 92.18% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x CD833627 (1-482)
 QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
 Db 157 CAGAAGTTGTGTGAGAGGCCAAGTGGGACATGTCAGGAGTTTGTGGAACAATAATGCG 216
 QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
 Db 217 TGTAAAGATCAGTGCATTCGATTCGAAAGACACATGATCTTGCACATATGCTTC 276
 QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
 Db 277 CCAGCTCACAAGTGTATCTGCTATTTCCCTTGT 309

RESULT 11
 CD833661
 LOCUS DEFINITION BN45.001C04F010914 BN45 Brassica napus cDNA clone BN45001C04, mRNA
 sequence.
 CD833661
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Brassica napus (rape)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 523)
 Genoplatte.
 Genoplatte, a major partnership french program in plant genomics
 Unpublished (2003)

```

COMMENT      Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com)
and http://genoplatte-info.infobiogen.fr).

FEATURES
source
1..523
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN4501C04"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Alignment Scores:
Pred. No.:      1,098-22      Length:      523
Score:          291.00      Matches:    47
Percent Similarity: 100.00%      Conservative: 4
Best Local Similarity: 92.18%      Mismatches: 0
Query Match:    100.00%      Indels:    0
DB:             14          Gaps:      0

SEQ9-X-AT-5-9-16-39 (1-51) x CD833661 (1-523)
Qy      1 GlnLysLeuCys***ArgProSer***ThrTpSerGlyValCys***AsnAsnAla 20
Db      139 CAGAAGCTGTGGAAAGCCAAAGTGGACGCGTGTGAGAGTCTGTGGAAACAATAATGCA 198
Qy      21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db      199 TGCAGAATCAGTGCATTCGACTAGAGAAAGCAGACATGATCTTGCACATATGCTTC 258
Qy      41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db      259 CCAGTCACAGTGCATCTGCTACTTCCTTGT 291

RESULT 12
CD828840
LOCUS      CD828840      543 bp      mRNA      linear      EST 10-JUL-2003
DEFINITION      EN40.040A33F011019 EN40 Brassica napus cDNA clone EN40040A23, mRNA
sequence.
ACCESSION      CD828840
VERSION      CD828840.1 GI:32510780
KEYWORDS
SOURCE      Brassica napus (rape)
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 543)
AUTHORS
TITLE      Genoplatte, a major partnership french program in plant genomics
JOURNAL      Unpublished (2003)
COMMENT      Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com)
and http://genoplatte-info.infobiogen.fr).

FEATURES
source
1..543
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="EN4004A23"

COMMENT      Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com)
and http://genoplatte-info.infobiogen.fr).

FEATURES
source
1..543
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="EN4004A23"

ORIGIN
Alignment Scores:
Pred. No.:      1,488-22      Length:      646
Score:          291.00      Matches:    47
Percent Similarity: 100.00%      Conservative: 4
Best Local Similarity: 92.16%      Mismatches: 0
Query Match:    100.00%      Indels:    0
DB:             14          Gaps:      0

SEQ9-X-AT-5-9-16-39 (1-51) x CD829429 (1-646)
Qy      1 GlnLysLeuCys***ArgProSer***ThrTpSerGlyValCys***AsnAsnAla 20
Db      138 CAGAAGCTGTGGAAAGCCAAAGTGGACGCGTGTGAGAGTCTGTGGAAACAATAATGCA 197
Qy      21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db      198 TGCAGAATCAGTGCATTCGACTAGAGAAAGCAGACATGATCTTGCACATATGCTTC 257
Qy      41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db      258 CCAGTCACAGTGCATCTGCTACTTCCTTGT 290

RESULT 13
CD829429
LOCUS      CD829429      646 bp      mRNA      linear      EST 10-JUL-2003
DEFINITION      EN40.042B06F011226 EN40 Brassica napus cDNA clone EN40042B06, mRNA
sequence.
ACCESSION      CD829429
VERSION      CD829429.1 GI:32511369
KEYWORDS
SOURCE      Brassica napus (rape)
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 646)
AUTHORS
TITLE      Genoplatte, a major partnership french program in plant genomics
JOURNAL      Unpublished (2003)
COMMENT      Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com)
and http://genoplatte-info.infobiogen.fr).

FEATURES
source
1..646
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/db_xref="taxon:3708"
/clone="EN40042B06"
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/clone_lib="BN40"

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Percent Similarity: 100.00%      Conservative: 4
Best Local Similarity: 92.16%      Mismatches: 0
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DB:             14          Gaps:      0

SEQ9-X-AT-5-9-16-39 (1-51) x CD829429 (1-646)
Qy      1 GlnLysLeuCys***ArgProSer***ThrTpSerGlyValCys***AsnAsnAla 20

```

| | | | |
|---|--|---|-----------------|
| Db | 132 | CAGAAGCTGTGCGAAAGCCCAAGTGGAAACGGTGTCAGGAGTCTGTGGAAAACAATAATGCA | 191 |
| Qy | 21 | CysLysAsnGlnCysIleAargLeuGluLysAlaAargHisGlySerCysAsnTyr****Phe | 40 |
| Db | 192 | TGCAGATCATGTCATTTCGACTAGAGAAACACGGCATGGATCTTGCACTATATGCTTC | 251 |
| Qy | 41 | ProAlaHisLysCysIleCysTyrPheProCys | 51 |
| Db | 252 | CCAGCTCACAGTGCATCTGCTACTTCCTTGT | 284 |
| RESULT 14 | | | |
| BZ517729 | | | |
| LOCUS | | | |
| DEFINITION | BZ517729 | 762 bp DNA linear | GSS 16-DEC-2000 |
| ACCESSION | BOMSG66TF | BO_2_3_KB Brassica oleracea genomic clone | BOMSG66, |
| VERSION | BZ517729 | genomic survey sequence. | |
| KEYWORDS | BZ517729.1 | GI:27048297 | |
| SOURCE | GSS. | | |
| ORGANISM | Brassica oleracea | | |
| | Brassica oleracea | | |
| | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | |
| | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; | | |
| | rosids; eurosids II; Brassicales; Brassicaceae; Brassica. | | |
| REFERENCE | 1 | (bases 1 to 762) | |
| AUTHORS | Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M. | | |
| TITLE | Whole genome shotgun sequencing of Brassica oleracea | | |
| JOURNAL | Unpublished (2001) | | |
| COMMENT | Other GSSs: BOMSG66TR | | |
| | Contact: Chris Town | | |
| | TIGR | | |
| | 9712 Medical Center Drive, Rockville, MD 20850, USA. | | |
| | Tel: 301-838-3523 | | |
| | Fax: 301-838-0208 | | |
| | Email: cdtown@tigr.org | | |
| | DNA is from a doubled haploid provided by Tom Osborn. | | |
| | Seq primer: TF | | |
| | Class: sheared ends. | | |
| FEATURES | | | |
| source | 1..762 | | |
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| | /mol_type="Genomic DNA" | | |
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| | /db_xref="taxon:3712" | | |
| | /clone="BOMSG66" | | |
| | /clone_lib="BO_2_3_KB" | | |
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| | genomic DNA inserted into pHOs1 using BstXI linkers" | | |
| ORIGIN | | | |
| Alignment Scores: | | | |
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| Query Match: | 100.00% | Indels: | 0 |
| DB: | 28 | Gaps: | 0 |
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| Qy | 1 | GlnLysLeuCys***ArgProSer***ThrTyrSerGlyValCys***AsnAsnAla | 20 |
| Db | 468 | CAGAAGCTGTGCGAAAGCCCAAGTGGAAACGGTGTCAGGAGTCTGTGGAAAACAATAATGCA | 527 |
| Qy | 21 | CysLysAsnGlnCysIleAargLeuGluLysAlaAargHisGlySerCysAsnTyr****Phe | 40 |
| Db | 528 | TGCAAGAATCAGTGCATCTGCACTAGAGAAACACGGCATGGATCTTGCACTATGCTTC | 588 |
| Qy | 41 | ProAlaHisLysCysIleCysTyrPheProCys | 51 |
| Db | 588 | CCAGCTCACAGTGCATCTGCTACTTCCTTGT | 620 |
| RESULT 15 | | | |

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 24, 2004, 03:45:35 ; Search time 405 Seconds
(without alignments)
534.958 Million cell updates/sec

Title: SEQ9-X-AT-5-9-16-39
Perfect score: 291
Sequence: 1 QKLCXRPSTWGVXNNNA.....RHGSCNYXPPAHKICICYPFC 51

Scoring table:
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bloms62DX -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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Database : N Geneseq 29Jan04:*
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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
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8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 291 | 100.0 | 261 | 2 AAQ38652 | AaQ38652 Rs-APP2 C |
| 2 | 291 | 100.0 | 288 | 2 AAQ70130 | AaQ70130 Antimicro |
| 3 | 291 | 100.0 | 434 | 3 AAZ99332 | Aaz99332 DNA encod |
| 4 | 291 | 100.0 | 437 | 3 AAZ99331 | Aaz99331 DNA encod |
| 5 | 291 | 100.0 | 443 | 3 AAZ99330 | Aaz99330 DNA encod |
| 6 | 291 | 100.0 | 446 | 3 AAZ99329 | Aaz99329 DNA encod |
| 7 | 291 | 100.0 | 449 | 3 AAAS3190 | AaAS3190 Raphanus |
| 8 | 291 | 100.0 | 485 | 3 AAZ99333 | Aaz99333 DNA encod |

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| 9 | 291 | 100.0 | 485 | 3 AAZ99335 | Aaz99335 DNA encod |
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| 13 | 291 | 100.0 | 534 | 3 AAZ51396 | Aaz51396 Portion o |
| 14 | 291 | 100.0 | 534 | 3 AAZ99327 | Aaz99327 DNA encod |
| 15 | 291 | 100.0 | 534 | 3 AAZ99325 | Aaz99325 DNA encod |
| 16 | 291 | 100.0 | 557 | 3 AAZ99336 | Aaz99336 DNA encod |
| 17 | 291 | 100.0 | 575 | 3 AAZ99339 | Aaz99339 DNA encod |
| 18 | 291 | 100.0 | 606 | 3 AAZ99326 | Aaz99326 DNA encod |
| 19 | 291 | 100.0 | 1093 | 3 AAZ99334 | Aaz99334 DNA encod |
| 20 | 286 | 98.3 | 394 | 2 ADC51221 | AdC51221 Brassica |
| 21 | 286 | 98.3 | 414 | 2 AAQ38650 | AaQ38650 Rs-APP1 C |
| 22 | 286 | 98.3 | 414 | 2 AAQ70128 | AaQ70128 Antimicro |
| 23 | 286 | 98.3 | 414 | 2 AA72333 | Aa72333 Raphanus |
| 24 | 286 | 98.3 | 414 | 2 AAT68696 | AaT68696 Radish an |
| 25 | 286 | 98.3 | 426 | 9 ADC51223 | AdC51223 Brassica |
| 26 | 281 | 96.6 | 243 | 7 ADA68378 | Ada68378 Arabidops |
| 27 | 281 | 96.6 | 403 | 2 AAV10632 | AaV10632 A. thalia |
| 28 | 269 | 92.4 | 308 | 2 AAT94577 | AaT94577 Cloned 5, |
| 29 | 261 | 89.7 | 243 | 6 ABZ14241 | AbZ14241 Arabidops |
| 30 | 261 | 89.7 | 243 | 7 ABZ42136 | AbZ42136 Arabidops |
| 31 | 261 | 89.7 | 400 | 2 AAV10633 | AaV10633 A. thalia |
| 32 | 261 | 89.7 | 1616 | 2 AAV10646 | AaV10646 A. thalia |
| 33 | 260 | 89.3 | 270 | 2 AAT94582 | AaT94582 Amplified |
| 34 | 260 | 89.3 | 286 | 2 AAT94574 | AaT94574 Alyssum s |
| 35 | 260 | 89.3 | 481 | 2 AAT93289 | AaT93289 Alyssum s |
| 36 | 259 | 83.0 | 243 | 6 ABQ82690 | AbQ82690 Wasabia j |
| 37 | 259 | 83.0 | 414 | 3 AAZ33123 | Aaz33123 Wasabia j |
| 38 | 258 | 88.7 | 500 | 2 AAT94581 | AaT94581 Composite |
| 39 | 254 | 87.3 | 243 | 6 ABQ82691 | AbQ82691 Wasabia j |
| 40 | 254 | 87.3 | 416 | 3 AAZ33124 | Aaz33124 Wasabia j |
| 41 | 217 | 74.6 | 1973 | 3 AAC46924 | Aac46924 Arabidops |
| 42 | 211 | 72.5 | 284 | 2 AAQ38651 | AaQ38651 Truncated |
| 43 | 211 | 72.5 | 284 | 2 AAQ70129 | AaQ70129 Antimicro |
| 44 | 201 | 63.1 | 306 | 2 AAT94580 | AaT94580 Cloned 3, |
| 45 | 160 | 55.0 | 658 | 5 AAAS4389 | AaAS4389 Plant def |

ALIGNMENTS

RESULT 1
AAQ38652
ID AAQ38652 standard; DNA; 261 BP.

XX AAQ38652;
XX
XX
DT 25-MAR-2003 (revised)
DT 07-JUL-1993 (first entry)
XX
DE Rs-APP2 CDNA.
XX
KW Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
KW fungicide; bactericide; antibiotic; antifungal; gram positive;
KW plant disease resistance; low toxicity.
XX
OS Raphanus sativus.
XX
XX Key Location/Qualifiers
FH CDS 16..256
FT /*tag= a

PN WO9305153-A1.
XX
PD 18-MAR-1993.
XX
FF 27-AUG-1992; 92WO-GB001570.
XX
PR 29-AUG-1991; 91GB-00018523.
PR 13-FEB-1992; 92GB-00003038.
PR 25-JUN-1992; 92GB-00013526.
XX
PA (ICIL) IMPERIAL CHEM IND PLC.


```

XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
PI Vanderleyden J;
XX WPI; 1993-100978/12.
XX Biotic proteins isolated from seeds of plants - e.g. brassica or
PT dahlia, useful for increasing plants' resistance to fungal and bacterial
PT diseases.
XX Example 21; Fig 35; 110pp; English.
XX This cDNA represents the sequence of Rs-APP2 from Raphanus sativus. PCR
CC primer AAQ38640 was used together with AAQ38641 to generate a probe for
CC screening a Raphanus sativus seed cDNA library. This primer corresponds
CC to amino acids 2 to 7 of Rs-APF1 and has a sense orientation. The 144bp
CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a
CC 123bp product, which was further reamplified with the same primers and
CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
CC product. This was used to screen a lambda ZAP11 cDNA library by in situ
CC plaque hybridisation. Positive plaques were purified and subjected to two
CC additional screening rounds with the same probe. Inserts were excised in
CC vivo into the pBluescript phagemid form with the aid of helper phage
CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and
CC their size compared by agarose gel electrophoresis. Four clones had
CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
CC of the 4 largest clones were then sequenced and found to differ only in
CC the length of their 5' and 3' UTR's. The longest sequence was identified
CC as Rs-APF1 (AAQ38650). Rs-APP2 was seen to differ by only 2 amino acids
CC from Rs-APF1, so the Rs-APF1 cDNA was transformed to the Rs-APP2
CC nucleotide sequence by PCR assisted site directed mutagenesis. (Updated
CC on 25-MAR-2003 to correct PN field.)
XX Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;
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Alignment Scores:
Pred. No.: 1,238-25 Length: 261
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
SEQ9-X-AT-5-9-16-39 (1-51) x AAQ38652 (1-261)
QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
Db 103 CAGAAAGTTGTGCGCAAGGCGCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCA 162
QY 21 CysLysAsnGlnCysTleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 163 TGCAGAAATCAGTGCATTAGACTTTGAAAGACACACATGATCTTGCACACTATGCTTTC 222
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 223 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
RESULT 2
AAQ70130
ID AAQ70130 standard; cDNA; 288 BP.
XX
AC AAQ70130;
XX
DT 25-MAR-2003 (revised)
DT 14-FEB-1995 (first entry)
XX Antimicrobial Rs-APP2.
XX Antimicrobial; Rs-APP2; symbiosis; disease-resistance; fungus-resistance;
KW Clavibacter xyl. subsp. cynodontis; Cxc; crop improvement; endophyte;
KW PCR; polymerase chain reaction; mutagenesis; ss.
XX Raphanus sativus.
OS

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XX WO9416076-A1.
XX 21-JUL-1994.
XX 05-JAN-1994; 94WO-GB000012.
XX 08-JAN-1993; 93GB-00000281.
XX (ZENE ) ZENECA LTD.
XX Dubock AC, Powell KA, Rees SB;
XX WPI; 1994-249223/30.
DR P-PSDB; AAR57327.
DR Antimicrobial protein producing endo-symbiotic microorganisms - is
PT produced by combining nucleic acids encoding the protein with an
PT endophyte, useful for protecting plant hosts from esp. fungal disease.
XX Disclosure; Page 33; 39pp; English.
XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
CC Clavibacter xyl. subsp. cynodontis (Cxc). Plants or seeds treated with
CC recombinant Cxc are protected against fungal disease. A suitable
CC antimicrobial protein is Rs-APF1 from R. sativus. The full-length cDNA
CC sequence of PCR assisted site-directed mutagenesis of Rs-APP2 is given in
CC AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1,4e-25 Length: 288
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
SEQ9-X-AT-5-9-16-39 (1-51) x AAQ70130 (1-288)
QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
Db 130 CAGAAAGTTGTGCGCAAGGCGCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCA 189
QY 21 CysLysAsnGlnCysTleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 190 TGCAGAAATCAGTGCATTAGACTTTGAAAGACACACATGATCTTGCACACTATGCTTTC 249
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 250 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 282
RESULT 3
AAZ99332
ID AAZ99332 standard; DNA; 434 BP.
XX
AC AAZ99332;
XX
DT 03-JUL-2000 (first entry)
XX
DE DNA encoding a fusion protein of DnaMPL and RsAPP2.
XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.
XX Synthetic.
OS Dahlia merckii.
OS Unidentified.
XX Key Location/Qualifiers
XX CDS 3..425

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FT /*tag= a
 FT /product= "fusion protein of DmAMP1 and RsAPP2"

XX WO200011175-A1.

XX 02-MAR-2000.

XX PF 17-AUG-1999; 99WO-GB002716.

XX PR 18-AUG-1998; 98GB-00018001.

XX PR 04-DEC-1998; 98GB-00026753.

XX (ZENE) ZENECA LTD.

XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;

XX WPI; 2000-246564/21.

XX P-PSDB; AAY84065.

XX Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.

XX Disclosure; Fig 27; 151pp; English.

XX The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polypeptide is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence.

XX SQ Sequence 434 BP; 108 A; 101 C; 117 G; 108 T; 0 U; 0 Other;

Alignment Scores:

| Pred. No.: | 2,426-25 | Length: | 434 |
|------------------------|----------|---------------|-----|
| Score: | 291.00 | Matches: | 47 |
| Percent Similarity: | 100.00% | Conservative: | 4 |
| Best Local Similarity: | 92.16% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99332 (1-434)

| QY | 1 | GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAla | 20 |
|----|-----|--|-----|
| DB | 270 | CAGAGTTGTGCCAAGGCCAAGTCGTACATGTCAGAGTCTGTGGAAACATACGCA | 329 |
| QY | 21 | CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe | 40 |
| DB | 330 | TGCAAGAATCAGTGTGATAGACTTTGAGAAACACGACATGATCTTGCACACTATCGTTTC | 389 |

QY 41 ProAlaHisLysCysIleCysTyr:PheProCys 51

DB 390 CCAGCTCACAGTGTATCTGCTACTTCTTGT 422

RESULT 4

ID AAZ99331

XX AAZ99331 standard; DNA; 437 BP.

XX AC AAZ99331;

XX 03-JUL-2000 (first entry)

XX DNA encoding a fusion protein of DmAMP1 and RsAPP2.

XX

KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
 KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.
 OS Synthetic.
 OS Dahlia merckii.
 OS Unidentified.

XX FH Key Location/Qualifiers

XX FT CDS 3..428

XX FT /*tag= a

XX FT /product= "fusion protein of DmAMP1 and RsAPP2"

XX PN WO200011175-A1.

XX PD 02-MAR-2000.

XX PF 17-AUG-1999; 99WO-GB002716.

XX PR 18-AUG-1998; 98GB-00018001.

XX PR 04-DEC-1998; 98GB-00026753.

XX (ZENE) ZENECA LTD.

XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;

XX WPI; 2000-246564/21.

XX P-PSDB; AAY84064.

XX Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.

XX Disclosure; Fig 26; 151pp; English.

XX The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polypeptide is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence.

XX SQ Sequence 437 BP; 109 A; 102 C; 118 G; 108 T; 0 U; 0 Other;

Alignment Scores:

| Pred. No.: | 2,44e-25 | Length: | 437 |
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| Best Local Similarity: | 92.16% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99331 (1-437)

| QY | 1 | GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAla | 20 |
|----|-----|---|-----|
| DB | 273 | CAGAGTTGTGCCAAGGCCAAGTCGTACATGTCAGAGTCTGTGGAAACATACGCA | 332 |

| QY | 21 | CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe | 40 |
|----|-----|--|-----|
| DB | 333 | TGCAAGAATCAGTGTGATAGACTTTGAGAAACACGACATGATCTTGCACACTATCGTTTC | 392 |

QY 41 ProAlaHisLysCysIleCysTyr:PheProCys 51

DB 393 CCAGCTCACAGTGTATCTGCTACTTCTTGT 425

RESULT 5

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AAZ99330
ID AAZ99330 standard; DNA; 443 BP.
XX
AC AAZ99330;
XX
DT 03-JUL-2000 (first entry)
XX
DE DNA encoding a fusion protein of DmAMP1 and RsAPP2.
XX
KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.
XX
OS Synthetic.
OS Dahlia merckii.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 3..434
FT FT /*tag= a
FT FT /product= "fusion protein of DmAMP1 and RsAPP2"
XX
FN WO200011175-A1.
XX
PD 02-MAR-2000.
XX
PF 17-AUG-1999; 99WO-GB002716.
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PR 18-AUG-1998; 98GB-00018001.
PR 04-DEC-1998; 98GB-00026753.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX
DR WPI; 2000-246564/21.
DR P-PSDB; AAY84063.
XX
PT Improving expression of polyproteins in plants involves coexpression of
PT two or more proteins in plants within a single transcription unit.
XX
PS Disclosure; Fig 25; 151pp; English.
XX
CC The present sequence encodes a protein of the invention, comprising the
CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
CC (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker
CC propeptide of the invention. The specification describes methods for
CC improving expression levels of one or more proteins in a transgenic
CC plant. The method comprises inserting a DNA sequence having a promoter
CC region operably linked to two or more protein encoding regions separated
CC by a DNA sequence coding for a linker propeptide and a terminator region.
CC The method is used to produce proteins in plants. The linker propeptide
CC comprising a cleavage site, whereby the expressed polypeptide is post-
CC translationally processed into the component protein molecules. The
CC propeptide sequence is rich in amino acids A, V, S and T and contains
CC dipeptidic sequences consisting of either two acidic, two basic or one
CC acidic and one basic residue as a cleavable linker sequence
XX
SQ Sequence 443 BP; 111 A; 102 C; 121 G; 109 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,49e-25 Length: 443
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99330 (1-443)

QY 1 GlyIysIeuCys**ArgProSer**ThrTrpSerGlyValCys***AsnAsnAla 20
DB 279 CAGAAGTTGTGCCAAGGCCAAGTCGTACATGCTCAGGAGTCTGTGGACACATACCGCA 338

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QY 21 CysIysIeuCysIleArgLeuGluValAlaArgHisGlySerCysAsnTy***Phe 40
DB 339 TGCAGATCATCGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 398

QY 41 ProAlaHisIysCysIleCysTyPheProCys 51
DB 399 CCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 431

RESULT 6
AAZ99329
ID AAZ99329 standard; DNA; 446 BP.
XX
AC AAZ99329;
XX
DT 03-JUL-2000 (first entry)
XX
DE DNA encoding a fusion protein of DmAMP1 and RsAPP2.
XX
KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.
XX
OS Synthetic.
OS Dahlia merckii.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 3..437
FT FT /*tag= a
FT FT /product= "fusion protein of DmAMP1 and RsAPP2"
XX
FN WO200011175-A1.
XX
PD 02-MAR-2000.
XX
PF 17-AUG-1999; 99WO-GB002716.
XX
PR 18-AUG-1998; 98GB-00018001.
PR 04-DEC-1998; 98GB-00026753.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX
DR WPI; 2000-246564/21.
DR P-PSDB; AAY84062.
XX
PT Improving expression of polyproteins in plants involves coexpression of
PT two or more proteins in plants within a single transcription unit.
XX
PS Disclosure; Fig 24; 151pp; English.
XX
CC The present sequence encodes a protein of the invention, comprising the
CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
CC (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker
CC propeptide of the invention. The specification describes methods for
CC improving expression levels of one or more proteins in a transgenic
CC plant. The method comprises inserting a DNA sequence having a promoter
CC region operably linked to two or more protein encoding regions separated
CC by a DNA sequence coding for a linker propeptide and a terminator region.
CC The method is used to produce proteins in plants. The linker propeptide
CC comprising a cleavage site, whereby the expressed polypeptide is post-
CC translationally processed into the component protein molecules. The
CC propeptide sequence is rich in amino acids A, V, S and T and contains
CC dipeptidic sequences consisting of either two acidic, two basic or one
CC acidic and one basic residue as a cleavable linker sequence
XX
SQ Sequence 446 BP; 111 A; 102 C; 123 G; 110 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,51e-25 Length: 446
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0

```

| | | | |
|---|---|--|-----|
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |
| SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99329 (1-446) | | | |
| QY | 1 | GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAla | 20 |
| DB | 282 | CAGAAGTTGTGCCAAGGCCAAGTCGACATGGTCAGAGTCTGTGGAAACAAATACGCA | 341 |
| QY | 21 | CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe | 40 |
| DB | 342 | TGCAAGATCAGTGCATTAGACTTTGAGAAAGCAGCAGATCGATCTTGCAACTATCGTTTC | 401 |
| QY | 41 | ProLalaHisLysCysIleCysTyrPheProCys | 51 |
| DB | 402 | CCAGCTCAAGTGTATCTGTACTTTCCTTGT | 434 |
| RESULT 7 | | | |
| AAAS3190 | AAAS3190 standard; DNA; 449 BP. | | |
| AC | AAAS3190; | | |
| DT | 06-OCT-2000 (first entry) | | |
| DE | Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1. | | |
| XX | Raphanus sativus; antibacterial; plant; resistance; paddy; radishin; | | |
| XX | pathogenic microbe; radish; rice blast disease; ds. | | |
| XX | Raphanus sativus. | | |
| XX | JP2000116379-A. | | |
| XX | 25-APR-2000. | | |
| XX | 09-OCT-1998; 98JP-00288472. | | |
| XX | 09-OCT-1998; 98JP-00288472. | | |
| XX | (TOYA-) TOYAMA KEN. | | |
| XX | WPI; 2000-389921/34. | | |
| XX | P-PSDB; AAY91117. | | |
| XX | Isolated DNA from Raphanus sativus used to transform a microbe and a | | |
| XX | plant to produce an antibacterial protein used to increase resistance of | | |
| XX | rice paddy against pathogenic microbes. | | |
| XX | Claim 1; Page 4; 7pp; Japanese. | | |
| XX | The present sequence encodes an antibacterial protein, designated | | |
| XX | radishin, isolated from Raphanus sativus (radish). A phage or plasmid | | |
| XX | comprising radishin can be used for increasing resistance of paddy and | | |
| XX | rice blast disease against pathogenic microbes | | |
| XX | Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other; | | |
| Alignment Scores: | | | |
| Pred. No.: | 2,53e-25 | Length: | 449 |
| Score: | 291.00 | Matches: | 47 |
| Percent Similarity: | 100.00% | Conservative: | 4 |
| Best Local Similarity: | 92.16% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |
| SEQ9-X-AT-5-9-16-39 (1-51) x AAAS3190 (1-449) | | | |
| QY | 1 | GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAla | 20 |
| DB | 128 | CAGAAGTTGTGTGACAGGCCAAGTCGACATGGTCAGAGTCTGTGGAAATATACGCA | 181 |
| QY | 21 | CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe | 40 |

| | | | |
|------------------------|--|---|-----|
| DB | 188 | TGCAGAAATCAGTCGATTCGACTTGGAGAAGCAGACATGGGTCTTTGCAACTATGCTTC | 247 |
| QY | 41 | ProblatislvsCyslleCysTyrPheProCys | 51 |
| DB | 248 | CCAGCTCACAAGTGATCTCTGTTATTTCCCTTGT | 280 |
| RESULT | 8 | | |
| ID | AAZ99333 | standard; DNA; 485 BP. | |
| AC | AAZ99333; | | |
| XX | | | |
| DT | 03-JUL-2000 | (first entry) | |
| DE | | | |
| XX | | | |
| XX | | | |
| KW | | DNA encoding a fusion protein of DmAMP1 and RsAFP2. | |
| KW | | Antimicrobial protein; AMPL; transgenic plant; linker propeptide; | |
| OS | | protein expression; plant defensin; RsAFP2; antifungal protein; APP2; ss. | |
| OS | | Synthetic. | |
| OS | | Dahlia merckii. | |
| OS | | Unidentified. | |
| XX | | | |
| XX | | | |
| XX | | Key Location/Qualifiers | |
| FT | CDS | 3..476 | |
| FT | | /*tag= a | |
| FT | | /product= "fusion protein of DmAMP1 and RsAFP2" | |
| XX | | | |
| XX | WO200011175-A1. | | |
| XX | | | |
| XX | 02-MAR-2000. | | |
| XX | | | |
| XX | 17-AUG-1999; | 99WB-GB002716. | |
| XX | 18-AUG-1998; | 98GB-00018001. | |
| PR | 04-DEC-1998; | 98GB-00025753. | |
| XX | | | |
| PA | (ZENE) ZENECA LTD. | | |
| XX | | | |
| PI | Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA; | | |
| XX | | | |
| DR | WPI; 2000-246564/21. | | |
| DR | P-PSDB; AA784066. | | |
| XX | | | |
| PT | Improving expression of polyproteins in plants involves coexpression of | | |
| PT | two or more proteins in plants within a single transcription unit. | | |
| XX | | | |
| PS | Disclosure; Fig 28; 151pp; English. | | |
| XX | | | |
| CC | The present sequence encodes a protein of the invention, comprising the | | |
| CC | mature proteins of the plant defensin, the Dahlia antimicrobial protein | | |
| CC | (AMP) 1 and the antifungal protein 2 (AP2), linked by a linker | | |
| CC | propeptide of the invention. The specification describes methods for | | |
| CC | improving expression levels of one or more proteins in a transgenic | | |
| CC | plant. The method comprises inserting a DNA sequence having a promoter | | |
| CC | region operably linked to two or more protein encoding regions separated | | |
| CC | by a DNA sequence coding for a linker propeptide and a terminator region | | |
| CC | The method is used to produce proteins in plants. The linker propeptide | | |
| CC | comprising a cleavage site whereby the expressed polypeptides are post- | | |
| CC | translationally processed into the component protein molecules. The | | |
| CC | propeptide sequence is rich in amino acids A, V, S and T and contains | | |
| CC | dipeptidic sequences consisting of either two acidic, two basic or one | | |
| CC | acidic and one basic residue as a cleavable linker sequence | | |
| XX | | | |
| SQ | Sequence 485 BP; 124 A; 107 C; 128 G; 126 T; 0 U; 0 Other; | | |
| Alignment Scores: | | | |
| Pred. No.: | 2,81e-25 | Length: | 485 |
| Score: | 291.00 | Matches: | 47 |
| Percent Similarity: | 100.00% | Conservative: | 4 |
| Best Local Similarity: | 92.16% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |

DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99333 (1-485)

Qy 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
 Db 321 CAGAAGTTGTGCCAAGGCCAAGTCGTACATGTCAGGAGTCTGTGGAAACAATAACGCA 380
 Qy 21 CysLysAsnGlnCysLeuLeuGluLeuAlaAaGcHisGlySerCysAsnTyr***Phe 40
 Db 381 TGCAGAATCAGTGCATTAAGCTTGAGAAAGCAGCAGATGGATCTTGCACATATCGTTTC 440

SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99335 (1-485)

Qy 41 ProAlaHisLysCysLeuCysTyrPheProCys 51
 Db 441 CCAGCTCACAAGTGTATCTGCTACTTCTTGT 473

RESULT 9
 AAZ99335
 ID AAZ99335 standard; DNA; 485 BP.
 XX AC AAZ99335;
 XX DT 03-JUL-2000 (first entry)
 XX DE DNA encoding a fusion protein of DmAMP1 and RsAPP2.
 XX KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
 XX KW protein expression; plant defensin; RsAPP2; antifungal protein; AFP2; ss.
 XX OS Synthetic.
 XX OS Dahlia merckii.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 XX FT CDS 3..476
 XX FT /*tag= a
 XX FT /product= "fusion protein of DmAMP1 and RsAPP2"
 XX PN WO200011175-A1.
 XX PD 02-MAR-2000.
 XX PP 17-AUG-1999; 99WO-GB002716.
 XX PR 18-AUG-1998; 98GB-00018001.
 XX PR 04-DEC-1998; 98GB-00026753.
 XX XX (ZENE) ZENECA LTD.
 XX PA Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
 XX PI WPI; 2000-246564/21.
 XX DR P-PSDB; AAY84069.
 XX XX Improving expression of polyproteins in plants involves coexpression of
 XX FT two or more proteins in plants within a single transcription unit.
 XX PS Disclosure; Fig 30; 151pp; English.
 XX CC The present sequence encodes a protein of the invention, comprising the
 XX CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
 XX CC (AMP) 1 and the antifungal protein 2 (RsAPP2), linked by a linker
 XX CC propeptide of the invention. The specification describes methods for
 XX CC improving expression levels of one or more proteins in a transgenic
 XX CC plant. The method comprises inserting a DNA sequence having a promoter
 XX CC region operably linked to two or more protein encoding regions separated
 XX CC by a DNA sequence coding for a linker propeptide and a terminator region.
 XX CC The method is used to produce proteins in plants. The linker propeptide
 XX CC comprising a cleavage site, whereby the expressed polypeptide is post-
 XX CC translationally processed into the component protein molecules. The
 XX CC propeptide sequence is rich in amino acids A, V, S and T and contains
 XX CC dipeptidic sequences consisting of either two acidic, two basic or one
 XX CC acidic and one basic residue as a cleavable linker sequence

XX SQ Sequence 485 BP; 139 A; 104 C; 128 G; 114 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,81e-25 Length: 485
 Score: 291.00 Matches: 47
 Percent Similarity: 100.00% Conservative: 4
 Best Local Similarity: 92.16% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

CC plant. The method comprises inserting a DNA sequence having a promoter
 CC region operably linked to two or more protein encoding regions separated
 CC by a DNA sequence coding for a linker propeptide and a terminator region.
 CC The method is used to produce proteins in plants. The linker propeptide
 CC comprising a cleavage site, whereby the expressed polypeptide is post-
 CC translationally processed into the component protein molecules. The
 CC propeptide sequence is rich in amino acids A, V, S and T and contains
 CC dipeptidic sequences consisting of either two acidic, two basic or one
 CC acidic and one basic residue as a cleavable linker sequence
 XX
 SQ Sequence 485 BP; 129 A; 106 C; 131 G; 119 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,81e-25 Length: 485
 Score: 291.00 Matches: 47
 Percent Similarity: 100.00% Conservative: 4
 Best Local Similarity: 92.16% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99337 (1-485)

QY 1 GlnLysLeuCys***ArgProSer***ThrTpsrGlyValCys***AsnAsnAla 20
 DB 321 CAGAGTTGTGCCAAGCCCAAGTCGACATGTCAGAGTCTGTGGAAACATACGCA 380
 QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
 DB 381 TGCAGAAATCAGTCAGTCATTAGACTTGAGAAAGCAGCAGATCTTGCAACTATCTGTTTC 440
 QY 41 ProLahisLysCysIleCysTyrPheProCys 51
 DB 441 CCAGTCAACAGTGTATCTGCTCTTCTTGT 473

RESULT 11

AAZ99338
 ID AAZ99338 standard; DNA; 488 BP.

AC AAZ99338;

DT 03-JUL-2000 (first entry)

DE DNA encoding a fusion protein of DmAMP1 and RsAFP2.

KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
 KW protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.

XX Synthetic.

OS Dahlia merckii.

OS Unidentified.

FX Key Location/Qualifiers

FT CDS 3..479

FT /*tag= a
 FT /product= "fusion protein of DmAMP1 and RsAFP2"

XX WO200011175-A1.

PN 02-MAR-2000.

XX 17-AUG-1999; 99WO-GB002716.

XX 18-AUG-1998; 98GB-00018001.

PR 04-DEC-1998; 98GB-00026753.

XX (ZENE) ZENECA LTD.

XX Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;

XX WPI; 2000-246564/21.

DR P-PSDB; AA84071.

XX Improving expression of polyproteins in plants involves coexpression of

PT two or more proteins in plants within a single transcription unit.

XX Disclosure; Fig 33; 151pp; English.

CC The present sequence encodes a protein of the invention, comprising the
 CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
 CC (AMP) 1 and the antifungal protein 2 (RsAFP2), linked by a linker
 CC propeptide of the invention. The specification describes methods for
 CC improving expression levels of one or more proteins in a transgenic
 CC plant. The method comprises inserting a DNA sequence having a promoter
 CC region operably linked to two or more protein encoding regions separated
 CC by a DNA sequence coding for a linker propeptide and a terminator region.
 CC The method is used to produce proteins in plants. The linker propeptide
 CC comprising a cleavage site, whereby the expressed polypeptide is post-
 CC translationally processed into the component protein molecules. The
 CC propeptide sequence is rich in amino acids A, V, S and T and contains
 CC dipeptidic sequences consisting of either two acidic, two basic or one
 CC acidic and one basic residue as a cleavable linker sequence
 XX
 SQ Sequence 488 BP; 117 A; 116 C; 131 G; 124 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,83e-25 Length: 488
 Score: 291.00 Matches: 47
 Percent Similarity: 100.00% Conservative: 4
 Best Local Similarity: 92.16% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99338 (1-488)

QY 1 GlnLysLeuCys***ArgProSer***ThrTpsrGlyValCys***AsnAsnAla 20
 DB 324 CAGAGTTGTGCCAAGCCCAAGTCGACATGTCAGAGTCTGTGGAAACATACGCA 383
 QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
 DB 384 TGCAGAAATCAGTCAGTCATTAGACTTGAGAAAGCAGCAGATCTTGCAACTATCTGTTTC 443
 QY 41 ProLahisLysCysIleCysTyrPheProCys 51
 DB 444 CCAGTCAACAGTGTATCTGCTCTTCTTGT 476

RESULT 12

AAZ99324
 ID AAZ99324 standard; DNA; 522 BP.

XX AAZ99324;

DT 03-JUL-2000 (first entry)

DE DNA encoding a fusion protein of DmAMP1 and RsAFP2.

KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
 KW protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.

XX Synthetic.

OS Dahlia merckii.

OS Unidentified.

FX Key Location/Qualifiers

FT misc_feature 160..309

FT /*tag= a
 FT /note= "encodes DmAMP1"

FT misc_feature 358..510

FT /*tag= b
 FT /note= "encodes RsAFP2"

XX WO200011175-A1.

XX 02-MAR-2000.

XX 17-AUG-1999; 99WO-GB002716.

```

XX 18-AUG-1998; 98GB-00018001.
PR 04-DEC-1998; 98GB-00026753.
XX (ZENE ) ZENECA LTD.
PA
XX Broekaert WF, Francois IEUA, De Boile MFC, Evans IJ, Ray JA;
XX
XX WPI; 2000-246564/21.
DR P-PSDB; AAY84057.
XX
XX Improving expression of polyproteins in plants involves coexpression of
PT two or more proteins in plants within a single transcription unit.
XX
XX Example 2; Fig 8; 151pp; English.
XX
XX The present sequence encodes a protein of the invention, comprising the
CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
CC (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker
CC propeptide of the invention. The specification describes methods for
CC improving expression levels of one or more proteins in a transgenic
CC plant. The method comprises inserting a DNA sequence having a promoter
CC region operably linked to two or more protein encoding regions separated
CC by a DNA sequence coding for a linker propeptide and a terminator region.
CC The method is used to produce proteins in plants. The linker propeptide
CC comprising a cleavage site whereby the expressed polypeptide is post-
CC translationally processed into the component protein molecules. The
CC propeptide sequence is rich in amino acids A, V, S and T and contains
CC dipeptidic sequences consisting of either two acidic, two basic or one
CC acidic and one basic residue as a cleavable linker sequence
XX
SQ Sequence 522 BP; 147 A; 119 C; 127 G; 129 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,098-25 Length: 522
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AA299324 (1-522)
QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAla 20
Db 358 CAGAAAGTTGTGCCAAAGGCCAAGTGGACATGCTCAGGAGTCTGTGGAACAATAACGCA 417
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTy***Phe 40
Db 418 TGCAAGAATCAGTGCATTAGACTTGAGAAAGCAGCATGGATCTTGCAACTATGCTTC 477
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 478 CCAGCTCACAAAGTGATCTGCTACTTCTCTGT 510

RESULT 13
AA251396
ID AA251396 standard; DNA; 534 BP.
XX
XX AA251396;
XX
XX 06-JUN-2000 (first entry)
XX
DE Portion of pFAJ3106 encoding Dahlia merckii antimicrobial protein.
XX
XX Antimicrobial protein; DnAMP; transgenic plant; microbial infection;
XX bacteria; fungi; field crop; fruit; vegetable; canola; banana; sunflower;
KW apple; plant transformation vector; ds.
XX
XX Dahlia merckii.
OS Synthetic.
XX
XX Key Location/Qualifiers

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CDS
FT 76..525
FT /*tag= a
FT /product= "Antimicrobial protein"
XX
XX WO200011196-A1.
XX
XX 02-MAR-2000.
XX
XX 17-AUG-1999; 99WO-GB002720.
XX
XX 18-AUG-1998; 98GB-00018003.
XX (ZENE ) ZENECA LTD.
XX
XX Evans IJ, Ray JA;
XX
XX WPI; 2000-237658/20.
DR P-PSDB; AAY70323.
XX
XX Polynucleotide sequences and expression products useful for producing
PT transgenic plants that are resistant to microbial infections.
XX
XX Example 3; Fig 7; 77pp; English.
XX
XX The present sequence corresponds to the region between XhoI and SacI
CC sites of plant transformation vector pFAJ3106, which encompass the coding
CC region for Dahlia merckii antimicrobial protein, Dn-AMP1. The vector is
CC useful in the production of transgenic plants which show improved
CC resistance to infections by microorganisms such as bacteria and fungi.
CC Transgenic plants include e.g. field crops, fruits and vegetables, such
CC as canola, sunflower, tomato, apple, banana, pear and mango
XX
XX Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,198-25 Length: 534
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AA251396 (1-534)
QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAla 20
Db 370 CAGAAAGTTGTGCCAAAGGCCAAGTGGACATGCTCAGGAGTCTGTGGAACAATAACGCA 429
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTy***Phe 40
Db 430 TGCAAGAATCAGTGCATTAGACTTGAGAAAGCAGCATGGATCTTGCAACTATGCTTC 489
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 490 CCAGCTCACAAAGTGATCTGCTACTTCTCTGT 522

RESULT 14
AA299327
ID AA299327 standard; DNA; 534 BP.
XX
XX AA299327;
XX
XX 03-JUL-2000 (first entry)
XX
DE DNA encoding a fusion protein of DnAMP1 and RsAPP2.
XX
XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.
XX
XX Synthetic.
OS Dahlia merckii.
OS Unidentified.
XX

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PH Key      Location/Qualifiers
FT CDS      76..522
FT          /*tag= a
FT misc_feature 162..309
FT          /*tag= b
FT          /note= "encodes DnAMP1"
FT misc_feature 372..519
FT          /*tag= c
FT          /note= "encodes RsAPP2"
XX WO200011175-A1.
XX PN
XX XX
XX PD 02-MAR-2000.
XX PF 17-AUG-1999; 99WO-GB002716.
XX PR 18-AUG-1998; 98GB-00018001.
XX PR 04-DEC-1998; 98GB-00026753.
XX PA (ZENE ) ZENECA LTD.
XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX DR WPI; 2000-246564/21.
XX DR P-PSDB; AAY84060.
XX XX
XX PT Improving expression of polyproteins in plants involves coexpression of
XX PT two or more proteins in plants within a single transcription unit.
XX PS Example 2; Fig 12; 15lpp; English.
XX CC The present sequence encodes a protein of the invention, comprising the
XX CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX CC (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker
XX CC propeptide of the invention. The specification describes methods for
XX CC improving expression levels of one or more proteins in a transgenic
XX CC plant. The method comprises inserting a DNA sequence having a promoter
XX CC region operably linked to two or more protein encoding regions separated
XX CC by a DNA sequence coding for a linker propeptide and a terminator region.
XX CC The method is used to produce proteins in plants. The linker propeptide
XX CC comprising a cleavage site, whereby the expressed polyprotein is post-
XX CC translationally processed into the component protein molecules. The
XX CC propeptide sequence is rich in amino acids A, V, S and T and contains
XX CC dipeptidic sequences consisting of either two acidic, two basic or one
XX CC acidic and one basic residue as a cleavable linker sequence
XX SQ Sequence 534 BP; 154 A; 120 C; 125 G; 135 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.19e-25 Length: 534
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AA299327 (1-534)
Qy 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
Db 370 CAGAAGTTGTGCCAAGCCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAAATAACGCA 429
Qy 21 CysLysAsnGlnCysIleAArgLeuGluLeuAlaArgHisGlySerCysAsnTyr***Phe 40
Db 430 TGCAAGATCAGTGCANTAGACTTGAGAAAGCAGACATGATGATCTTGCACTATGCTTC 489
Qy 41 ProLhisLysCysIleCysTyrPheProCys 51
Db 490 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 522

RESULT 15
AAZ99325
ID AA299325 standard; DNA; 534 BP.

```

```

XX AA299325;
XX AC
XX XX
XX DT 03-JUL-2000 (first entry)
XX DE DNA encoding a fusion protein of DnAMP1 and RsAPP2.
XX KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
XX KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.
XX OS Synthetic.
XX OS Dahlia merckii.
XX OS Unidentified.
XX PH Location/Qualifiers
XX FT 76..522
XX FT /*tag= a
XX FT misc_feature 160..309
XX FT /*tag= b
XX FT /*note= "encodes DnAMP1"
XX FT misc_feature 370..538
XX FT /*tag= c
XX FT /*note= "encodes RsAPP2"
XX PN WO200011175-A1.
XX XX
XX PD 02-MAR-2000.
XX PF 17-AUG-1999; 99WO-GB002716.
XX PR 18-AUG-1998; 98GB-00018001.
XX PR 04-DEC-1998; 98GB-00026753.
XX PA (ZENE ) ZENECA LTD.
XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX DR WPI; 2000-246564/21.
XX DR P-PSDB; AAY84058.
XX XX
XX PT Improving expression of polyproteins in plants involves coexpression of
XX PT two or more proteins in plants within a single transcription unit.
XX PS Example 2; Fig 9; 15lpp; English.
XX CC The present sequence encodes a protein of the invention, comprising the
XX CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX CC (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker
XX CC propeptide of the invention. The specification describes methods for
XX CC improving expression levels of one or more proteins in a transgenic
XX CC plant. The method comprises inserting a DNA sequence having a promoter
XX CC region operably linked to two or more protein encoding regions separated
XX CC by a DNA sequence coding for a linker propeptide and a terminator region.
XX CC The method is used to produce proteins in plants. The linker propeptide
XX CC comprising a cleavage site, whereby the expressed polyprotein is post-
XX CC translationally processed into the component protein molecules. The
XX CC propeptide sequence is rich in amino acids A, V, S and T and contains
XX CC dipeptidic sequences consisting of either two acidic, two basic or one
XX CC acidic and one basic residue as a cleavable linker sequence
XX SQ Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.19e-25 Length: 534
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.18% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AA299325 (1-534)
Qy 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20

```



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Db 370 CAGAACTTGTGCAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACAAATACCCA 429
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 430 TCAAAGAATCAGTGCATTAGACTTGAGAAAGCAGACATGGATCTTGCACACTATGCTCTTC 489
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 490 CCAGCTCACAAGTGTATCTGCTACTTCTTCTTGT 522
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Search completed: March 24, 2004, 05:57:25
Job time : 411 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 24, 2004, 05:44:19 ; Search time 82 Seconds

(without alignments)
345.152 Million cell updates/sec

Title: SEQ9-X-AT-5-9-16-39

Perfect score: 291

Sequence: 1 QKLCXRSXTWSGVGXNNNA.....RHGSCNYXFFAHKICVFFPC 51

Scoring table: BLQSUM62DX

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/cgn2_1/USPTO_epool/ROBINSON1006252/runat_23032004_112103_24824/app_query.fasta_1.19
-DB=Issued Patents NA -QWMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blcsum62DX -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=ROBINSON1006252@cgn2_1_69@runat_23032004_112103_24824 -NCPUG=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:

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4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 291 | 100.0 | 285 | 1 | US-08-627-706-17 |
| 2 | 291 | 100.0 | 285 | 3 | US-09-103-489-17 |
| 3 | 291 | 100.0 | 285 | 4 | US-09-829-381D-17 |
| 4 | 291 | 100.0 | 288 | 1 | US-08-377-687-58 |
| 5 | 291 | 100.0 | 288 | 3 | US-08-777-192-58 |
| 6 | 291 | 100.0 | 288 | 3 | US-08-971-982-58 |
| 7 | 286 | 98.3 | 285 | 1 | US-08-627-706-16 |
| 8 | 286 | 98.3 | 285 | 3 | US-09-103-489-16 |
| 9 | 286 | 98.3 | 285 | 4 | US-09-829-381D-16 |
| 10 | 286 | 98.3 | 414 | 1 | US-08-377-687-48 |
| 11 | 286 | 98.3 | 414 | 1 | US-08-777-192-48 |
| 12 | 286 | 98.3 | 414 | 3 | US-08-971-982-48 |

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| 13 | 286 | 98.3 | 414 | 4 | US-09-077-951-19 | Sequence 19, Appl |
| 14 | 286 | 98.3 | 414 | 4 | US-09-077-948A-45 | Sequence 45, Appl |
| 15 | 289 | 92.4 | 308 | 1 | US-08-627-706-5 | Sequence 5, Appl |
| 16 | 269 | 92.4 | 308 | 3 | US-09-103-489-5 | Sequence 5, Appl |
| 17 | 269 | 92.4 | 308 | 4 | US-09-829-381D-5 | Sequence 5, Appl |
| 18 | 260 | 89.3 | 270 | 1 | US-08-627-706-14 | Sequence 14, Appl |
| 19 | 260 | 89.3 | 270 | 3 | US-09-103-489-14 | Sequence 14, Appl |
| 20 | 260 | 89.3 | 270 | 4 | US-09-829-381D-14 | Sequence 14, Appl |
| 21 | 260 | 89.3 | 286 | 1 | US-08-627-706-12 | Sequence 12, Appl |
| 22 | 260 | 89.3 | 286 | 3 | US-09-103-489-12 | Sequence 12, Appl |
| 23 | 260 | 89.3 | 286 | 4 | US-09-829-381D-12 | Sequence 12, Appl |
| 24 | 258 | 88.7 | 500 | 1 | US-08-627-706-9 | Sequence 9, Appl |
| 25 | 258 | 88.7 | 500 | 3 | US-09-103-489-9 | Sequence 9, Appl |
| 26 | 258 | 88.7 | 500 | 4 | US-09-829-381D-9 | Sequence 9, Appl |
| 27 | 211 | 72.5 | 284 | 1 | US-08-377-687-50 | Sequence 50, Appl |
| 28 | 211 | 72.5 | 284 | 3 | US-08-777-192-50 | Sequence 50, Appl |
| 29 | 211 | 72.5 | 284 | 3 | US-08-971-982-50 | Sequence 50, Appl |
| 30 | 201 | 69.1 | 306 | 1 | US-08-627-706-8 | Sequence 8, Appl |
| 31 | 201 | 69.1 | 306 | 3 | US-09-103-489-8 | Sequence 8, Appl |
| 32 | 201 | 69.1 | 306 | 4 | US-09-829-381D-8 | Sequence 8, Appl |
| 33 | 150 | 51.5 | 150 | 1 | US-08-377-687-31 | Sequence 31, Appl |
| 34 | 150 | 51.5 | 150 | 1 | US-08-777-192-31 | Sequence 31, Appl |
| 35 | 150 | 51.5 | 150 | 3 | US-08-971-982-31 | Sequence 31, Appl |
| 36 | 147 | 50.5 | 150 | 1 | US-08-377-687-34 | Sequence 34, Appl |
| 37 | 147 | 50.5 | 150 | 1 | US-08-777-192-34 | Sequence 34, Appl |
| 38 | 147 | 50.5 | 150 | 3 | US-08-971-982-34 | Sequence 34, Appl |
| 39 | 145 | 49.8 | 150 | 1 | US-08-377-687-33 | Sequence 33, Appl |
| 40 | 145 | 49.8 | 150 | 1 | US-08-777-192-33 | Sequence 33, Appl |
| 41 | 145 | 49.8 | 150 | 3 | US-08-971-982-33 | Sequence 33, Appl |
| 42 | 142 | 48.8 | 565 | 4 | US-09-589-733C-6 | Sequence 6, Appl |
| 43 | 136.5 | 46.9 | 147 | 1 | US-08-377-687-36 | Sequence 36, Appl |
| 44 | 136.5 | 46.9 | 147 | 1 | US-08-777-192-36 | Sequence 36, Appl |
| 45 | 136.5 | 46.9 | 147 | 3 | US-08-971-982-36 | Sequence 36, Appl |

ALIGNMENTS

RESULT 1

US-08-627-706-17
; Sequence 17, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BBAF
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 17:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-08-627-706-17

Alignment Scores:
Pred. No.: 4,86e-28 Length: 285
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-08-627-706-17 (1-285)
QY 1 GlnLysLeuCys***ArgProSer***ThrTTPSerGlyValCys***AsnAsnAsnAla 20
Db 118 CAAAAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGGGAAACACACACGCA 177
QY 21 CysLysAsnGlnCysIleAArgLeuGluLysAlaAArgHisGlySerCysAsnTyr***Phe 40
Db 178 TGAAGAACAATGCAATGCATCAGACTCGAAGGACGCGCATGGATCTTGCAACTACGTCCTTC 237
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 238 CCAGCTCACAAGTGCAATCTGCTACTTCCATGC 270

RESULT 2
US-08-103-489-17
; Sequence 17, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,489
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: other nucleic acid

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; DESCRIPTION: /desc = "synthetic DNA"
US-09-103-489-17

Alignment Scores:
Pred. No.: 4,86e-28 Length: 285
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-103-489-17 (1-285)
QY 1 GlnLysLeuCys***ArgProSer***ThrTTPSerGlyValCys***AsnAsnAsnAla 20
Db 118 CAAAAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGGGAAACACACACGCA 177
QY 21 CysLysAsnGlnCysIleAArgLeuGluLysAlaAArgHisGlySerCysAsnTyr***Phe 40
Db 178 TGAAGAACAATGCAATGCATCAGACTCGAAGGACGCGCATGGATCTTGCAACTACGTCCTTC 237
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 238 CCAGCTCACAAGTGCAATCTGCTACTTCCATGC 270

RESULT 3
US-09-829-381D-17
; Sequence 17, Application US/09829381D
; Patent No. 6653280
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
; TITLE OF INVENTION: Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 17
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-829-381D-17

Alignment Scores:
Pred. No.: 4,86e-28 Length: 285
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-829-381D-17 (1-285)
QY 1 GlnLysLeuCys***ArgProSer***ThrTTPSerGlyValCys***AsnAsnAsnAla 20
Db 118 CAAAAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGGGAAACACACACGCA 177
QY 21 CysLysAsnGlnCysIleAArgLeuGluLysAlaAArgHisGlySerCysAsnTyr***Phe 40
Db 178 TGAAGAACAATGCAATGCATCAGACTCGAAGGACGCGCATGGATCTTGCAACTACGTCCTTC 237
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 238 CCAGCTCACAAGTGCAATCTGCTACTTCCATGC 270

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RESULT 4
 US-08-377-687-58
 ; Sequence 58, Application US/08377687
 ; Patent No. 5538525
 ; GENERAL INFORMATION:
 ; APPLICANT: BROEKART, WILLEM F.
 ; APPLICANT: CAMMUE, BRUNO P.A.
 ; APPLICANT: OSBORN, RUPERT W.
 ; APPLICANT: REES, SARAH B.
 ; APPLICANT: TERRAS, FRANKY R.G.
 ; APPLICANT: VANDERLEYDEN, JOZEF
 ; TITLE OF INVENTION: BIOCIDAL PROTEINS
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DABY & CUSHMAN
 ; STREET: 1100 NEW YORK AVENUE, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/377,687
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/002,480
 ; FILING DATE: 04-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOKULIS, PAUL N.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-861-3000
 ; TELEFAX: 202-822-0944
 ; INFORMATION FOR SEQ ID NO: 58:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 288 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 43..282
 ; US-08-377-687-58

Alignment Scores: 4.93e-28 Length: 288
 Pred. No.: 291.00 Matches: 47
 Score: 100.00% Conservative: 4
 Percent Similarity: 100.00%
 Best Local Similarity: 92.16% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

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| QY | 1 | GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAspAla | 20 |
| DB | 130 | CAGAAGTTGTGCCAAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCA | 189 |
| QY | 21 | CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe | 40 |
| DB | 190 | TGCAAGATCACTGCATTAGACTTGAGAAAGCAGCATGGATCTTGCAACTATGCTTC | 249 |
| QY | 41 | ProAlaHisLysCysIleCysTyrPheProCys | 51 |
| DB | 250 | CCAGCTCACAGTGTATCTGCTACTTTCCTTGT | 282 |

RESULT 5
 US-08-777-192-58
 ; Sequence 58, Application US/08777192
 ; Patent No. 5624869
 ; GENERAL INFORMATION:
 ; APPLICANT: BROEKART, WILLEM F.
 ; APPLICANT: CAMMUE, BRUNO P.A.
 ; APPLICANT: OSBORN, RUPERT W.
 ; APPLICANT: REES, SARAH B.
 ; APPLICANT: TERRAS, FRANKY R.G.
 ; APPLICANT: VANDERLEYDEN, JOZEF
 ; TITLE OF INVENTION: BIOCIDAL PROTEINS
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DABY & CUSHMAN
 ; STREET: 1100 NEW YORK AVENUE, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/777,192
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 06/002,480
 ; FILING DATE: 04-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOKULIS, PAUL N.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-861-3000
 ; TELEFAX: 202-822-0944
 ; INFORMATION FOR SEQ ID NO: 58:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 288 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 43..282
 ; US-08-777-192-58

Alignment Scores: 4.93e-28 Length: 288
 Pred. No.: 291.00 Matches: 47
 Score: 100.00% Conservative: 4
 Percent Similarity: 100.00%
 Best Local Similarity: 92.16% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-08-777-192-58 (1-288)

| | | | |
|----|-----|--|-----|
| QY | 1 | GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla | 20 |
| DB | 130 | CAGAAGTTGTGCCAAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCA | 189 |
| QY | 21 | CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe | 40 |
| DB | 190 | TGCAAGATCACTGCATTAGACTTGAGAAAGCAGCATGGATCTTGCAACTATGCTTC | 249 |
| QY | 41 | ProAlaHisLysCysIleCysTyrPheProCys | 51 |
| DB | 250 | CCAGCTCACAGTGTATCTGCTACTTTCCTTGT | 282 |

RESULT 6

US-08-971-982-58
; Sequence 58, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKHAERT, WILLEM F.
; CAMMUE, BRUNO P.A.
; OSBORN, RUPERT W.
; REES, SARAH B.
; TERRAS, FRANKY R.G.
; VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BICCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,982
; FILING DATE: 17-NO. 6187904-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURES:
; NAME/KEY: CDS
; LOCATION: 43..282
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-08-971-982-58

Alignment Scores:
Pred. No.: 4 93e-28 Length: 288
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-08-971-982-58 (1-288)

| | | |
|----|-----|--|
| QY | 1 | GLNLYSLEUCYS***ARGPROSER***THRTPSERGLYVALCYS***ASNASNANALA 20 |
| DB | 130 | CAGAAGTTGTCACAAAGGCGCAAGTGGGACATGGTCAGGAGTCTGTGGAAACCAATACCGCA 189 |
| QY | 21 | CYSLYSASNGLNCYSILEARGLEUGLUYSALAARGHISGLYSERCYSASNTYR***PHE 40 |
| DB | 190 | TGCAAGATCAGTGCAATAGATTGAGAAAGCAGCATGGATCTTGCACATATGCTTTC 249 |
| QY | 41 | PROLAHISLYSCYSILECYSTYRPHETPCYS 51 |
| DB | 250 | CCAGCTCACAAAGTGATCTGCTACTTTCCTTGT 282 |

RESULT 7

US-08-627-706-16
; Sequence 16, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-08-627-706-16

Alignment Scores:
Pred. No.: 2 06e-27 Length: 285
Score: 286.00 Matches: 46
Percent Similarity: 98.04% Conservative: 4
Best Local Similarity: 90.20% Mismatches: 1
Query Match: 98.28% Indels: 0
DB: 1 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-08-627-706-16 (1-285)

| | | |
|----|-----|---|
| QY | 1 | GLNLYSLEUCYS***ARGPROSER***THRTPSERGLYVALCYS***ASNASNANALA 20 |
| DB | 118 | CAAAAGTTGTCGAGAGAGCCATCAGGACCTTGTCAGGAGTCTGCGGAAACAACACGCA 177 |
| QY | 21 | CYSLYSASNGLNCYSILEARGLEUGLUYSALAARGHISGLYSERCYSASNTYR***PHE 40 |
| DB | 178 | TGCAAGAACCAATGCATCAACCTCGAGAAGCGCAGGCATGGATCTTGCACATAGCTTTC 237 |
| QY | 41 | PROLAHISLYSCYSILECYSTYRPHETPCYS 51 |
| DB | 238 | CCAGCTCACAGTGCATCTGCTACTTTCATGC 270 |

RESULT 8

US-09-103-489-16
; Sequence 16, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:

APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, B44F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-09-103-489-16

Alignment Scores:
Pred. No.: 2,068-27 Length: 285
Score: 286.00 Matches: 46
Percent Similarity: 99.04% Conservative: 4
Best Local Similarity: 90.20% Mismatches: 1
Query Match: 98.28% Indels: 0
DB: Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-103-489-16 (1-285)

QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
Db 118 CAAAAGTTGTGGAGAGGCCATCAGGACTTGGTCAGGAGTCTGGGAAACAAACACGCA 177
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 178 TCAGAAGCAACATGATCACTCAACCTCGAGAGGACCGCATGTGATCTTGCACACTAGCTCTTC 237
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 238 CCAGCTCACAAGTGCATCTGCTACTTCCATGC 270

RESULT 9

US-09-829-381D-16
Sequence 16, Application US/09829381D
Patent No. 6653280

GENERAL INFORMATION:

APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.

APPLICANT: Wu, Yonnie S.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
TITLE OF INVENTION: Plant Pathogenic Fungi

FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 285

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-829-381D-16

Alignment Scores:
Pred. No.: 2,068-27 Length: 285
Score: 286.00 Matches: 46
Percent Similarity: 99.04% Conservative: 4
Best Local Similarity: 90.20% Mismatches: 1
Query Match: 98.28% Indels: 0
DB: Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-829-381D-16 (1-285)

QY 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
Db 118 CAAAAGTTGTGGAGAGGCCATCAGGACTTGGTCAGGAGTCTGGGAAACAAACACGCA 177
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 178 TCAGAAGCAACATGATCACTCAACCTCGAGAGGACCGCATGTGATCTTGCACACTAGCTCTTC 237
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 238 CCAGCTCACAAGTGCATCTGCTACTTCCATGC 270

RESULT 10

US-08-377-687-48
Sequence 48, Application US/08377687
Patent No. 5538525

GENERAL INFORMATION:

APPLICANT: BROEKERT, WILLEM F.

APPLICANT: CAMMUE, BRUNO P.A.

APPLICANT: OSBORN, RUPERT W.

APPLICANT: REES, SARAH B.

APPLICANT: TERRAS, FRANKI R.G.

APPLICANT: VANDERLEYDEN, JOZEF

TITLE OF INVENTION: BIOCIDAL PROTEINS

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARRY & CUSHMAN

STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/377,687

FILING DATE:

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/002,480

FILING DATE: 04-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 99042/SBE.36525/US/A

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..255
US-08-377-687-48

Alignment Scores:
Pred. No.: 3,45e-27 Length: 414
Score: 286.00 Matches: 46
Percent Similarity: 98.04% Conservative: 4
Best Local Similarity: 90.20% Mismatches: 1
Query Match: 98.28% Indels: 0
DB: 1 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-08-377-687-48 (1-414)

QY 1 GlnLysLeuCys***ArgProSer***ThrTpsrGlyValCys***AsnAsnAala 20
Db 103 CAGAAGTTGTGGAAAGGCCAAGTGGACATGCTCAGGAGTCTGTGGAAACATATACGCA 162
QY 21 CysLysAsnGlnCysLeuArgLeuGlnLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 163 TGAAGAATCAGTGCATTACCTTGAGAAAGCAGCATGATCTTGAACCTATGCTTC 222
QY 41 ProAlaHisLysCysLeuCysTyrPheProCys 51
Db 223 CCAGCTCACAAGTGATCTGCTACTTCTCTGT 255

RESULT 11

US-08-777-192-48
Sequence 48, Application US/08777192
Patent No. 5824869
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBAY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..255
US-08-777-192-48

Alignment Scores:
Pred. No.: 3,45e-27 Length: 414
Score: 286.00 Matches: 46
Percent Similarity: 98.04% Conservative: 4
Best Local Similarity: 90.20% Mismatches: 1
Query Match: 98.28% Indels: 0
DB: 1 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-08-777-192-48 (1-414)

QY 1 GlnLysLeuCys***ArgProSer***ThrTpsrGlyValCys***AsnAsnAala 20
Db 103 CAGAAGTTGTGGAAAGGCCAAGTGGACATGCTCAGGAGTCTGTGGAAACATATACGCA 162
QY 21 CysLysAsnGlnCysLeuArgLeuGlnLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 163 TGAAGAATCAGTGCATTACCTTGAGAAAGCAGCATGATCTTGAACCTATGCTTC 222
QY 41 ProAlaHisLysCysLeuCysTyrPheProCys 51
Db 223 CCAGCTCACAAGTGATCTGCTACTTCTCTGT 255

RESULT 12

US-08-971-982-48
Sequence 48, Application US/08971982
Patent No. 6187904
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBAY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,982
FILING DATE: 17-NO. 6187904-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

| | | | |
|--|-----|--|-----|
| Db | 103 | CAGAAGTTGTGCGAAGGCCCAAGTGGACATGGTTCAGAGTCTGTGTGAAACAATAACGCA | 162 |
| Qy | 21 | CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe | 40 |
| Db | 163 | TGCAGATTCAGTGCATTAACCTTGAGAAAGCAGACATGGATCTTGCACATATGCTTC | 222 |
| Qy | 41 | ProAlaHisLysCysIleCysTyrPheProCys | 51 |
| Db | 223 | CCAGCTCAAGTGTATCTGCTACTTCTTCTTGT | 255 |
| RESULT 14 | | | |
| US-09-077-948A-45 | | | |
| ; Sequence 45, Application US/09077948A | | | |
| ; Patent No. 6605698 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Van Amerongen, Aart | | | |
| ; APPLICANT: Fant, Franky | | | |
| ; APPLICANT: Borremans, Frans | | | |
| ; APPLICANT: De Samblanx, Genoveva | | | |
| ; APPLICANT: Sijtsma, Lolke | | | |
| ; APPLICANT: Melloen, Robbert | | | |
| ; APPLICANT: Puijk, Wouter | | | |
| ; APPLICANT: Schaaper, Wilhelmus | | | |
| ; APPLICANT: Broekaert, Willem | | | |
| ; APPLICANT: Van Gelder, Wilhelmus | | | |
| ; APPLICANT: Rees, Sarah | | | |
| ; TITLE OF INVENTION: Antifungal Proteins | | | |
| ; FILE REFERENCE: 109846-257(SYN-035) | | | |
| ; CURRENT APPLICATION NUMBER: US/09/077,948A | | | |
| ; CURRENT FILING DATE: 1998-08-07 | | | |
| ; PRIOR APPLICATION NUMBER: PCT/GB96/03068 | | | |
| ; PRIOR FILING DATE: 1996-12-12 | | | |
| ; PRIOR APPLICATION NUMBER: GB 9606552.9 | | | |
| ; PRIOR FILING DATE: 1996-03-28 | | | |
| ; PRIOR APPLICATION NUMBER: GB 9525455.3 | | | |
| ; PRIOR FILING DATE: 1995-12-13 | | | |
| ; NUMBER OF SEQ ID NOS: 141 | | | |
| ; SOFTWARE: FastSeq for Windows Version 4.0 | | | |
| ; SEQ ID NO 45 | | | |
| ; LENGTH: 414 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Raphanus sativus | | | |
| US-09-077-948A-45 | | | |
| Alignment Scores: | | | |
| Pred. No.: 3,45e-27 Length: 414 | | | |
| Score: 286.00 Matches: 46 | | | |
| Percent Similarity: 98.04% Conservative: 4 | | | |
| Best Local Similarity: 90.20% Mismatches: 1 | | | |
| Query Match: 98.28% Indels: 0 | | | |
| DB: Gaps: 0 | | | |
| SEQ9-X-AT-5-9-16-39 (1-51) x US-09-077-948A-45 (1-414) | | | |
| Qy | 1 | GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAla | 20 |
| Db | 103 | CAGAAGTTGTGCGAAGGCCCAAGTGGACATGGTTCAGAGTCTGTGTGAAACAATAACGCA | 162 |
| Qy | 21 | CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe | 40 |
| Db | 163 | TGCAGATTCAGTGCATTAACCTTGAGAAAGCAGACATGGATCTTGCACATATGCTTC | 222 |
| Qy | 41 | ProAlaHisLysCysIleCysTyrPheProCys | 51 |
| Db | 223 | CCAGCTCAAGTGTATCTGCTACTTCTTCTTGT | 255 |
| RESULT 15 | | | |
| US-08-627-706-5 | | | |
| ; Sequence 5, Application US/08627706 | | | |
| ; Patent No. 5773696 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Liang, Jihong | | | |


```

; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-627-706-5

```

```

Alignment Scores:
Pred. No.:      3.09e-25      Length:      308
Score:          269.00      Matches:      43
Percent Similarity: 94.12%      Conservative: 5
Best Local Similarity: 84.31%      Mismatches: 3
Query Match:      92.44%      Indels:      0
DB:               1          Gaps:      0

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SEQ9-X-AT-5-9-16-39 (1-51) x US-08-627-706-5 (1-308)

```

Qy      1  GlnLysLeuCys**ArgProSer***ThrTrpSerGlyValCys**AsnAsnAsnAla 20
Db      156 CGAAGTTGCGAGAGTCCAGTGGAAACATGGTCAGGCGTGTGGAAACACACATGCT 215
Qy      21  CysLysAsnGlnCysLeuArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db      216 TGAAGAATCAGTGCATTAACCTTGAAGGAGCNCGACATGGATCTTGCACACTATGTCCTC 275
Qy      41  ProAlaHisLysCysLeuTyrPheProCys 51
Db      276 CCAGCTCACAAGTGCAATGCTACTTCCCTGT 308

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Search completed: March 24, 2004, 07:42:49
Job time : 92 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 24, 2004, 04:48:26 ; Search time 2998 Seconds
(without alignments)
737.323 Million cell updates/sec

Title: SEQ9-X-AT-5-9-16-39

Perfect score: 291

Sequence: 1 QKLCXRPSTWGSVCXNNNA.....RHGSCNYXPPAHKICICYFPC 51

Scoring table: BLOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

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-O=/cgn2_1/USPTO_spool/ROBINSON1006252/runat_23032004_112102_24796/app_query.fasta_1.19
-DB=GenEmbl -QFMT=fastcap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62DX -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=ROBINSON1006252@cgn_1_13731@runat_23032004_112102_24796 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*

29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.rod.*
36: em.htg.mam.*
37: em.htg.vrt.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|-------|-------|--------|----|-----------|--------------------|
| 1 | 291 | 100.0 | 285 | 6 | AR014693 | AR014693 Sequence |
| 2 | 291 | 100.0 | 285 | 6 | AR432393 | AR432393 Sequence |
| 3 | 291 | 100.0 | 288 | 6 | A39553 | A39553 Sequence 41 |
| 4 | 291 | 100.0 | 288 | 6 | AR050161 | AR050161 Sequence |
| 5 | 291 | 100.0 | 288 | 6 | AR130280 | AR130280 Sequence |
| 6 | 291 | 100.0 | 288 | 6 | I23736 | I23736 Sequence 58 |
| 7 | 291 | 100.0 | 434 | 6 | BD223242 | BD223242 Method of |
| 8 | 291 | 100.0 | 437 | 6 | BD223241 | BD223241 Method of |
| 9 | 291 | 100.0 | 443 | 6 | BD223240 | BD223240 Method of |
| 10 | 291 | 100.0 | 446 | 6 | BD223239 | BD223239 Method of |
| 11 | 291 | 100.0 | 449 | 6 | E34290 | E34290 Phage and p |
| 12 | 291 | 100.0 | 457 | 8 | RSU18556 | U18556 Raphanus sa |
| 13 | 291 | 100.0 | 485 | 6 | BD223243 | BD223243 Method of |
| 14 | 291 | 100.0 | 485 | 6 | BD223245 | BD223245 Method of |
| 15 | 291 | 100.0 | 485 | 6 | BD223247 | BD223247 Method of |
| 16 | 291 | 100.0 | 488 | 6 | BD223248 | BD223248 Method of |
| 17 | 291 | 100.0 | 522 | 6 | BD223233 | BD223233 Method of |
| 18 | 291 | 100.0 | 534 | 6 | BD240936 | BD240936 Polynucle |
| 19 | 291 | 100.0 | 534 | 6 | BD223234 | BD223234 Method of |
| 20 | 291 | 100.0 | 534 | 6 | BD223237 | BD223237 Method of |
| 21 | 291 | 100.0 | 557 | 6 | BD223246 | BD223246 Method of |
| 22 | 291 | 100.0 | 575 | 6 | BD223249 | BD223249 Method of |
| 23 | 291 | 100.0 | 606 | 6 | BD223236 | BD223236 Method of |
| 24 | 291 | 100.0 | 933 | 8 | BOL311046 | AJ311046 Brassica |
| 25 | 291 | 100.0 | 1093 | 6 | BD223244 | BD223244 Method of |
| 26 | 286 | 98.3 | 285 | 6 | AR014692 | AR014692 Sequence |
| 27 | 286 | 98.3 | 285 | 6 | AR432392 | AR432392 Sequence |
| 28 | 286 | 98.3 | 335 | 8 | RSU18557 | U18557 Raphanus sa |
| 29 | 286 | 98.3 | 414 | 6 | A26875 | A26875 R.sativus A |
| 30 | 286 | 98.3 | 414 | 6 | A39549 | A39549 Sequence 37 |
| 31 | 286 | 98.3 | 414 | 6 | A63404 | A63404 Sequence 19 |
| 32 | 286 | 98.3 | 414 | 6 | AR050153 | AR050153 Sequence |
| 33 | 286 | 98.3 | 414 | 6 | AR130272 | AR130272 Sequence |
| 34 | 286 | 98.3 | 414 | 6 | I23728 | I23728 Sequence 48 |
| 35 | 286 | 98.3 | 414 | 6 | AR207337 | AR207337 Sequence |
| 36 | 286 | 98.3 | 414 | 6 | AR374914 | AR374914 Sequence |
| 37 | 281 | 96.6 | 243 | 6 | AX412406 | AX412406 Sequence |
| 38 | 281 | 96.6 | 243 | 6 | AX412601 | AX412601 Sequence |
| 39 | 281 | 96.6 | 243 | 6 | AX651878 | AX651878 Sequence |
| 40 | 281 | 96.6 | 243 | 8 | AY060506 | AY060506 Arabidops |
| 41 | 281 | 96.6 | 403 | 6 | A68645 | A68645 Sequence 13 |
| 42 | 281 | 96.6 | 403 | 8 | ATANTSPC | X91916 A.thaliana |
| 43 | 281 | 96.6 | 425 | 8 | AY052236 | AY052236 Arabidops |
| 44 | 281 | 96.6 | 471 | 11 | BV010672 | BV010672 MASC STS1 |
| 45 | 281 | 96.6 | 563 | 11 | BV010667 | BV010667 MASC STS1 |

ALIGNMENTS

RESULT 1

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AR014693
LOCUS AR014693 285 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 17 from patent US 5773696.
ACCESSION AR014693
VERSION AR014693.1 GI:3972147
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 285)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide alyAPP from Alyssum and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 5773696-A 17 30-JUN-1998;
FEATURES
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Score: 291.00 Matches: 47
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Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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QY 1 GlnLysLeuCys**ArgProSer**ThrTpSerGlyValCys**AsnAsnAla 20
Db 118 CAAAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGGGAAACAACACGCA 177

QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 178 TGAAGAACCAATGCATCAGACTCGAAGAGGACGCGCATGGATCTTGCACATACGCTTTC 237

QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 238 CCAGCTCACAAGTGCATCTGCTACTTCCATGC 270

RESULT 2
AR432393
LOCUS AR432393 285 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 17 from patent US 6653280.
ACCESSION AR432393
VERSION AR432393.1 GI:40194670
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 285)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide alyAPP from Alyssum and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 17 25-NOV-2003;
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 4,97e-25 Length: 285
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AR432393 (1-285)

QY 1 GlnLysLeuCys**ArgProSer**ThrTpSerGlyValCys**AsnAsnAla 20
Db 118 CAAAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGGGAAACAACACGCA 177

QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 178 TGAAGAACCAATGCATCAGACTCGAAGAGGACGCGCATGGATCTTGCACATACGCTTTC 237

QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 238 CCAGCTCACAAGTGCATCTGCTACTTCCATGC 270

RESULT 2
AR432393
LOCUS AR432393 285 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 17 from patent US 6653280.
ACCESSION AR432393
VERSION AR432393.1 GI:40194670
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 285)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide alyAPP from Alyssum and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 17 25-NOV-2003;
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ORIGIN
Alignment Scores:
Pred. No.: 4,97e-25 Length: 285
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AR432393 (1-285)

QY 1 GlnLysLeuCys**ArgProSer**ThrTpSerGlyValCys**AsnAsnAla 20
Db 118 CAAAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGGGAAACAACACGCA 177

QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 178 TGAAGAACCAATGCATCAGACTCGAAGAGGACGCGCATGGATCTTGCACATACGCTTTC 237

QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 238 CCAGCTCACAAGTGCATCTGCTACTTCCATGC 270

RESULT 2
AR432393
LOCUS AR432393 285 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 17 from patent US 6653280.
ACCESSION AR432393
VERSION AR432393.1 GI:40194670
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 285)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide alyAPP from Alyssum and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 17 25-NOV-2003;
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        Location/Qualifiers
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Alignment Scores:
Pred. No.: 4,97e-25 Length: 285
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AR432393 (1-285)

QY 1 GlnLysLeuCys**ArgProSer**ThrTpSerGlyValCys**AsnAsnAla 20
Db 118 CAAAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGGGAAACAACACGCA 177

QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 178 TGAAGAACCAATGCATCAGACTCGAAGAGGACGCGCATGGATCTTGCACATACGCTTTC 237

QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 238 CCAGCTCACAAGTGCATCTGCTACTTCCATGC 270

RESULT 3
A39553
LOCUS A39553 288 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 41 from Patent WO9416076.
ACCESSION A39553
VERSION A39553.1 GI:2295844
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 288)
AUTHORS Dubock,A.C., Powell,K.A. and Rees,S.B.
TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
JOURNAL Patent: WO 9416076-A 41 21-JUL-1994;
COMMENT ZENECA LTD (GB)
FEATURES
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Alignment Scores:
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Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x A39553 (1-288)

QY 1 GlnLysLeuCys**ArgProSer**ThrTpSerGlyValCys**AsnAsnAla 20
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QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 190 TGAAGAACCAATGCATCAGACTTGAAGAGGACGCGCATGGATCTTGCACATACGCTTTC 249

QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 250 CCAGCTCACAAGTGCATCTGCTACTTCCATGC 282

RESULT 4
AR050161
LOCUS AR050161 288 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 58 from patent US 5824869.
ACCESSION AR050161
VERSION AR050161.1 GI:5972153
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 288)
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B., Terras,F.R.G. and Vanderleyden,J.
TITLE Bioticidal proteins
JOURNAL Patent: US 5824869-A 58 20-OCT-1998;
FEATURES
    Location/Qualifiers

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need to be fixed

Gly

100

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Sequence 58 from patent US 538525.
123736.1 GI:1603606
Unknown.
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 288)
Broekaert W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
JOURNAL
Patent: US 538525-A 58 23-JUL-1996;
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
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Best Local Similarity: 92.18% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
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130 CAGAAGTTGTGCAAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAACATAACGCA 189
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
190 TGCAGAATCATGTCATAGACTTGGAGAAAGCAGACATGGATCTTGCAACTATGCTTTC 249
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
250 CCAGCTCACAAGTGTATCTGCTACTTCTCTTGT 282
RESULT 7
BD223242 434 bp DNA linear PAT 17-JUL-2003
LOCUS
Method of genetic expression of polypeptide in plant.
BD223242
BD223242.1 GI:33033012
JP 2002523047-A/11.
synthetic construct
artificial construct
artificial sequences.
1 (bases 1 to 434)
Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and
Ray, J.A.
Method of genetic expression of polypeptide in plant
Patent: JP 2002523047-A 11 30-JUL-2002;
SYNGENTA LTD
OS Artificial Sequence
PN JP 2002523047-A/11
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566429
PR 18-AUG-1998 GB 9818001.1, 04-DEC-1998 GB 9826753.7 PI
WILLEM FRANS BROEKAERT, ISABELLE ELISA JEANNE
AUGUSTINE FRANCOIS,
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI.
ANTHONY RAY
PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02// (C12N5/10, PC
C12R1:91)
PC C12N15/00, C12N5/00, (C12N5/00, C12R1:91)
CC Description of Artificial Sequence: Synthetic sequence FH
Key CDS Location/Qualifiers
FT CDS (3)..(425).
FEATURES
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source

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RESULT 10
BD223239
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Syngenta LTD
PN JP 2002523047-A/8
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566429
PR 18-AUG-1998 GB 9818001.1,04-DEC-1998 GB 9826753.7 PI
WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
AUGUSTINE FRANCOIS,
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
ANTHONY RAY
PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02, (C12N5/10, PC
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PC C12N15/00, C12N5/00, (C12N5/00, C12R1:91)
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Location/Qualifiers
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Percent Similarity: 100.00% Conservative: 4
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x BD223239 (1-446)

QY 1 GlnLysLeuCys***ArgProSer***ThrTpSerGlyValCys***AsnAsnAla 20
Db 282 CAGAAGTTGTGCCAAGGCCAAGTCGTACATGTCAGGAGTCGTGGAAACAATAACGCA 341
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 342 TGCAGGATCATGTCATGATGACTTGCAGAAAGCACACATGATGCTTCAACTATCGTTTC 401
QY 41 ProLalaHisLysCysIleCysTyrPheProCys 51
Db 402 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 434

RESULT 11
E34290
LOCUS
DEFINITION
Phage and plasmid constructed by ligating antibacterial protein
gene DNA with vector DNA, transformant microorganism and
transformant plant containing the same and antibacterial protein.
E34290
ACCESSION
E34290.1 GI:18624295
VERSION
E34290.1
KEYWORDS
JP 2000116379-A/1.
SOURCE
unidentified
ORGANISM
unclassified.

REFERENCE
E34290
AUTHORS
TITLE
JOURNAL
COMMENT
OS Syngenta LTD
PN JP 2002523047-A/8
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566429
PR 18-AUG-1998 GB 9818001.1,04-DEC-1998 GB 9826753.7 PI
WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
AUGUSTINE FRANCOIS,
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
ANTHONY RAY
PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02, (C12N5/10, PC
C12R1:91),
PC C12N15/00, C12N5/00, (C12N5/00, C12R1:91)
CC Description of Artificial Sequence: Synthetic sequence FH
Key Location/Qualifiers
FT CDS
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Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred No.: 8,45e-25 Length: 446
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x E34290 (1-449)

QY 1 GlnLysLeuCys***ArgProSer***ThrTpSerGlyValCys***AsnAsnAla 20
Db 128 CAGAAGTTGTGTGCACAGGCCAAGTCGGCATGTCAGAGTCGTGGAAATATTAACGCA 187
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 188 TGCAGGATCATGTCATGATGACTTGCAGAAAGCACACATGATGCTTCAACTATCGTTTC 247
QY 41 ProLalaHisLysCysIleCysTyrPheProCys 51
Db 248 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 280

RESULT 12
RSU18556
LOCUS
DEFINITION
Raphanus sativus antifungal protein 2 preprotein (Rs-AFP2) mRNA,
complete cds.
ACCESSION
RSU18556
VERSION
U18556.1
KEYWORDS
GI:609319
SOURCE
Raphanus sativus (radish)
ORGANISM
Raphanus sativus
Raphanus sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.

REFERENCE
1 (sites)
TERRAS, F.R.G., Eggermont, K., Kovaleva, V., Raikhel, N.V.,
Osborn, R.W., Kester, A., Rees, S., Torrekens, S., Van Leuven, F.,
Vanderleyden, J., Cammue, B.P.A. and Broekaert, W.F.
Small cysteine-rich antifungal proteins from radish: their role in
host defense
Plant Cell 7, 568-573 (1995)
2 (bases 1 to 457)
TERRAS, F.R.
Direct Submission
Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory

REFERENCE
1 (bases 1 to 449)
Shoji, K.
Phage and plasmid constructed by ligating antibacterial protein
gene DNA with vector DNA, transformant microorganism and
transformant plant containing the same and antibacterial protein
Patent: JP 2000116379-A 1 25-APR-2000;
TOYAMA PREF
OS Raphanus sativus L.
PN JP 2000116379-A/1
PD 25-APR-2000
PF 09-OCT-1998 JP 1998288472
PR KAZUAKI SHOJI
PC C12N15/09, A01H5/00, C07K14/415, C12N1/21, C12N5/10, C12R1:91, PC
C12N15/00, (C12N1/21, C12R1:91), (C12N5/10, C12R1:91), PC
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PC C12N5/00, C12R1:91), (C12N5/00, C12R1:91) CC
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ORIGIN
Alignment Scores:
Pred No.: 8,52e-25 Length: 449
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x E34290 (1-449)

QY 1 GlnLysLeuCys***ArgProSer***ThrTpSerGlyValCys***AsnAsnAla 20
Db 128 CAGAAGTTGTGTGCACAGGCCAAGTCGGCATGTCAGAGTCGTGGAAATATTAACGCA 187
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 188 TGCAGGATCATGTCATGATGACTTGCAGAAAGCACACATGATGCTTCAACTATCGTTTC 247
QY 41 ProLalaHisLysCysIleCysTyrPheProCys 51
Db 248 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 280

RESULT 12
RSU18556
LOCUS
DEFINITION
Raphanus sativus antifungal protein 2 preprotein (Rs-AFP2) mRNA,
complete cds.
ACCESSION
RSU18556
VERSION
U18556.1
KEYWORDS
GI:609319
SOURCE
Raphanus sativus (radish)
ORGANISM
Raphanus sativus
Raphanus sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.

REFERENCE
1 (sites)
TERRAS, F.R.G., Eggermont, K., Kovaleva, V., Raikhel, N.V.,
Osborn, R.W., Kester, A., Rees, S., Torrekens, S., Van Leuven, F.,
Vanderleyden, J., Cammue, B.P.A. and Broekaert, W.F.
Small cysteine-rich antifungal proteins from radish: their role in
host defense
Plant Cell 7, 568-573 (1995)
2 (bases 1 to 457)
TERRAS, F.R.
Direct Submission
Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory

```

of Genetics, Applied Biological Sciences, W. De Croylaan 42,
Heverlee, Belgium, B-3001

Location/Qualifiers

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/tissue_type="seed"

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/genes="Rs-AFP2"

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/codon_start=1

/evidence=experimental

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/protein_id="AAA69340.1"

/db_xref="GI:609320"

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GNNAACNQICIRLEKARHGSCNYVFAHKICVFC"

42. .128

/genes="Rs-AFP2"

129. .281

/genes="Rs-AFP2"

/products="antifungal protein 2"

/function="antifungal, fungistatic"

/note="Evidence for antifungal activity: Analysis of two
novel classes of antifungal proteins from radish (Raphanus
sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
Chem. 267, 15301-15309"

/citation=[1]

/evidence=experimental

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Pred. No.: 8.7e-25 Length: 457

Score: 291.00 Matches: 47

Percent Similarity: 100.00% Conservative: 4

Best Local Similarity: 92.16% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0

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Db 129 CAGAAGTTGTGTACAGAGCCCAAGTGGGACATGTCAGAGCTCTGTGGAAATAATAACGCA 188

QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40

Db 189 TGCAGAATCAGTGCATTTCGACTTGAAAGCAGCATGGTGGCTTTCGAACTATGCTTC 248

QY 41 ProLahHisLysCysIleCysTyrPheProCys 51

Db 249 CCAGCTCACAAGTGTATCTGTTATTTCCCTGT 281

RESULT 13

LOCUS BD223243 485 bp DNA linear PAT 17-JUL-2003

DEFINITION Method of genetic expression of polyprotein in plant.

ACCESSION BD223243

VERSION BD223243.1 GI:33033013

KEYWORDS JP 2002523047-A/12.

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 485)

AUTHORS Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.

TITLE Method of genetic expression of polyprotein in plant

JOURNAL Patent: JP 2002523047-A 12 30-JUL-2002;

SYNGENTA LTD

Key CDS Location/Qualifiers
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 Qy 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
 Db 381 TGCAGAAATCAGTGCATAGACATTGAGAAGCAGCAGATGGATCTTGCAACTATCGTTTC 440
 Qy 41 ProAlaHisLysCysIleCysTyrPheProCys 51
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RESULT 15

BD223247 485 bp DNA linear PAT 17-JUL-2003
 LOCUS
 DEFINITION Method of genetic expression of polyprotein in plant.
 ACCESSION BD223247
 VERSION BD223247.1 GI:33033017
 KEYWORDS JP 2002523047-A/16.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1 (bases 1 to 485)
 AUTHORS Broekaert,W.F., Francois,I.E.J.A., Bolle,M.F.C.D., Evans,I.J. and Ray,J.A.

TITLE Method of genetic expression of polyprotein in plant
 JOURNAL Patent: JP 2002523047-A 16 30-JUL-2002;
 SYNGENTA LTD
 COMMENT OS Artificial Sequence
 PN JP 2002523047-A/16
 PD 30-JUL-2002
 PF 17-AUG-1999 JP 2000566429
 PR 18-AUG-1998 GB 9818001.1,04-DEC-1998 GB 9826753.7 PI
 WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
 AUGUSTINE FRANCOIS
 PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
 ANTHONY RAY
 PC C12N15/09,A01H1/00,C07K1/12,C12N5/10,C12P21/02//C12N5/10, PC
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FEATURES
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ORIGIN

Alignment Scores:
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 Percent Similarity: 100.00% Conservative: 4

Best Local Similarity: 92.16% Mismatches: 0
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 Db 321 CAGAAAGTTGTGCCAAAGGCCAAGTCGTACATGGTCAGGAGTCTGTGGAAACAATAACGCA 380
 Qy 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
 Db 381 TGCAGAAATCAGTGCATAGACATTGAGAAGCAGCAGATGGATCTTGCAACTATCGTTTC 440
 Qy 41 ProAlaHisLysCysIleCysTyrPheProCys 51
 Db 441 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 473

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